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February 21, 2003, 07:40:25 ; Search time 102 Seconds
(without alignments)
1371.061 Million cell updates/sec
                                                                                                                                    /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
                                                                                                                                                                                                                   884236
5.1.4_p5_4578
Compugen Ltd.
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                                                                                                                                                                                           442118 segs, 280819700 residues
version 5 - 2003 C
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Maximum Match 100%
Listing first 45 summaries
                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                       US-09-936-145-1
249
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                                                                                                            Title:
Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		% Query				
- :	Score	Match	Match Length DB	DB	QI	Description
	242.8	97.5	2084	σ	US-09-918-543-9	Sequence 9, Appli
٠.	242.8	97.5	2084	10	US-09-769-864-58	Sequence 58, Appl
	242.8	97.5	2084	10	US-09-854-346-9	Sequence 9, Appli
	107	43.0	6837	6	US-09-928-847B-49	Sequence 49, Appl
	36	14.5	383	10	US-09-969-347-299	Sequence 299, App
	34.2	13.7	309	10	US-09-974-300-1061	Sequence 1061, Ap
~	34	13.7	640681	10	US-09-790-988-1	Sequence 1, Appli
~	33.8	13.6	882	6	US-09-983-802-133	Sequence 133, App
_	33.8	13.6	10716	10	US-09-954-456-270	Sequence 270, App
_	33.4	13.4	516	10	US-09-864-761-7942	Sequence 7942, Ap
	33.4	13.4	640681	10	US-09-790-988-1	Sequence 1, Appli
۵.	33	13.3		10	US-09-834-975-451	Sequence 451, App
_	32.8	13.2	2405	6	US-09-764-868-1458	Sequence 1458, Ap
	32.8	13.2		σ	US-09-764-868-1459	Sequence 1459, Ap
	32.8	13.2	9224	6	US-10-108-605-254	Sequence 254, App
	32.8	13.2	18449	6	US-09-764-868-1457	
_	32.8	13.2	28588	10	US-09-764-887-399	Sequence 399, App
	32.4	13.0	18692	10	US-09-764-847-1682	Sequence 1682, Ap
_	32.4	13.0	197496	σ	US-09-877-177-10	Sequence 10, Appl

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1 GCCCCGCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTGATGACGATGATTTGG 60

61

Appli 00, Ap 21, Ap 27, Ap 27, Ap Appl (21, Appl (31, Appl (65, Appl (65, Appl (65, Appl (65, Appl (65, Appl (65, Appl (65, Appl (65, Appl (65, Appl (66, Appl (67, Appl (67, Appl (68, Appl		0;
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		Gaps
Sequence 4 Sequence 3 Sequence 3 Sequence 5 Sequence 6 Sequence 6 Sequence 6 Sequence 6 Sequence 7 Sequence 7 Sequence 7 Sequence 7 Sequence 7 Sequence 8	properties	2084;
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US-09-754-853A-4 US-09-938-842A-4550 US-09-938-842A-3562 US-09-938-842A-3562 US-09-938-842A-3562 US-09-938-842A-3562 US-09-880-107-1627 US-10-060-763-12 US-09-864-761-16211 US-09-864-761-16454 US-09-864-761-16454 US-09-954-456-124 US-09-974-8877-958 US-09-764-8877-958 US-09-764-8877-956 US-09-764-847-1965 US-09-864-161-12921 US-09-89-161-12921 US-09-189-561-53 US-09-789-561-79 US-09-789-561-79 US-09-925-301-164 US-09-933-797-82	ALIGNMENTS 1543 22ymes A/S 16 mutants with altered 17 11 12 inciens	Score 242.8; DB 9; Pred. No. 3.8e-53;); Mismatches 2;
	09918 S S S S S S S S S S S S S S S S S S S	28.3
513509 5200 5200 953 31124 31124 31124 538 9121 235 225 1120 8995 510 783 2163 394 510 783 783 783 783 783 783 783 783 783 783	ALIG Application US/09918543 Application US/09918543 RMATION: No. US20020155574Alozymes Thisted, Thomas Kjaerulff, Soren Andersen, Carsten Andersen, Carsten Fuglsang, Claus Crone VENTION: Alpha-amylase mut VENTION: 10062.200-05 LICATION NUMBER: US/09/918 LICATION NUMBER: US/09/918 EQ ID NOS: 30 atentin version 3.1 84 Bacillus amyloliquefaciens CDS (343)(1794) RMATION:	97.5%; larity 99.2%; Conservative
0.000 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Applicat Applicat S2002015 SEMATION: UCSO Thisted Adersel Frg1san VENTION: NCET 10N LICATION: NCET 10N LING DATE SEQ 1D NO atentin 884 Bacillus (CDS (343)(nilarit
######################################	AND SEPTEMBLY OF AND SEPTEMBLY OF SEPTEMBLY	Query Match Best Local Similarity Matches 244; Conser
010202020202020202020202020202020202020	RESULT 1 US-09-918-5. Sequence. Sequence. Retent No. General II APPLICAN TITLE OF FILE FILE CURRENT INGRENT INGRENT CURRENT CURRENT INGRAFE CORGANIS FEATURE INGRAFE INGRA	Query M Best Lo Matches
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121 ATCAGACAGGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGAATAAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCCCCGCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTGATGACGACTGATTTGG 60
                                                                                                                                                                                                                                                                                                                                                     1 GCCCCGCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTTGATGACTGATGTTTGG 60
                                                                                                                                                                                                                                                                                                                                     DB 10; Length 2084;
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (669)..(669)
OTHER INFORMATION: n denotes an undetermined nucleotide
                                                                                                                                                                                                                                            Score 242.8; DB 10;
Pred. No. 3.8e-53;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jorgensen, Steen T
APPLICANT: Rasmussen, Michael D
APPLICANT: Andersen, Jens Tonne
APPLICANT: Olsen, Carsten
TITLE OF INVENTION: Multiple Insertion of Genes
FILE REPERENCE: 10022.204 'US
CURRENT APPLICANTON NUBBER: US/09/928,847B
CURRENT FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin version 3.1
SEQ ID NO 49
LENGTH: 6837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 43.0%; Score 107; DB 9; I Best Local Similarity 100.0%; Pred. No. 2.8e-18; Matches 107; Conservative 0; Mismatches 0;
 CURRENT APPLICATION NUMBER: US/09/854,346
                                                                                                     TYPE: DNA
ORGANISM: Bacillus amyloliquefaciens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Plasmid pMOL 1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49, Application US/09928847B Publication No. US20030032186A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: No. US20030032186Alozymes
              CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                               97.5%;
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                                                                                                                                                                                                                                              Query Match 97.5
Best Local Similarity 99.2
Matches 244; Conservative
                                                                                                                                                        : NAME/KEY: CDS
: LOCATION: (343)..(1794)
: OTHER INFORMATION: BAN
US-09-854-346-9
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AGAGGA 246
                                                 SOFTWARE: Pater
SEQ ID NO 9
LENGTH: 2084
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181 GGGGGCTTGTTATTTTTACTGATATGTAAATTATAATTTGTATAAGAAATGAGAGGG 240
                  GGGGGGTTGTTATTATTTACTGATATGTAAAATATAATTTGTATAAGAAAATGAGAGGG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Svendsen, Allan
APPLICANT: Jorgensen, Christel Thea
APPLICANT: Nielsen, Bjarne Ronfeldt
TITLE OF INVENTION: Alpha e maylase variants with altered 1,6 activity
FILE REFERENCE: 6140.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2084;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.5%; Score 242.8; DB 10;
99.2%; Pred. No. 3.8e-53;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                       APPLICANT: SVORGESON, ALLEN V.
APPLICANT: SVORGESON, ALLEN V.
APPLICANT: Andersen, Carsten
APPLICANT: Mielsen, Bjarne
APPLICANT: Mielsen, Torben L.
APPLICANT: Missen, Torben L.
APPLICANT: Kjaerulff, Soren
TITLE REFERENCE: 5368 200-US
CURRENT FILING DATE: 2001-01-25
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 58
LENGTH: 2084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 9, Application US/09854346
; Patent No. US/202068352A1
; GENERAL INFORMATION:
; APPLICANT: No. US/20020068352A10zymes A/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Bacillus amyloliquefaciens
                                                                                                                                                                                         Sequence 58, Application US/09769864 Patent No. US20010039253A1
                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (343)...(1794)
US-09-769-864-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                         HIIIII
AGAGGA 246
                                                                   241 AGAGGA 246
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                                                                                                                                                        RESULT 2
US-09-769-864-58
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Matches 244;
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US-09-854-346-9
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                                                                                                     241
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                                                          140 ATGCTGTCCAGACTGTCCGCTGTGTAAAAAATAAGGAATAAAGGGGGGGTTGTTATTTT 199
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Length 6837;
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83 TGAGAAAAGAAGACCATAAAAATACCTTGTCTGTCATCAGACAGGGTATTTTTATG 142
                                                                GCCCCGCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTGATGACTGATGTGG 60
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CURRENT APPLICATION NUMBER: US/09/983,802

CURRENT FILING DATE: 2001-10-25

CURRENT FILING DATE: 2001-10-25

PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08

PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08

PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-07

PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-07

PRIOR PLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926

PRIOR PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929

PRIOR PRILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR PLING DATE: EARLIER FILING DATE: 1997-07-08
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                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANBE, HIDEMI
APPLICANT: HATAORI, MASAHIRA
APPLICANT: SARAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0129
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR PAPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEO ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
                                                                                                                                                                                                  274 TCCAAGAGATCGACGAGCTTTTCCGAAAAAGAAGA 308
                                                                                                                                             61 CTGAAGAAGTGGATCGATTGTTGAGAAAGAAGA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 1
Pred. No. 44;
0; Mismatches
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Publication No. US20030022185A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09790988
Patent No. US20020127687A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.7%;
59.2%;
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SEQ ID NO 1
LENGTH: 640681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.7
Best Local Similarity 59.2
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Buchnera sp. US-09-790-988-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-983-802-133
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                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signaturity Cancer Gene Determination and Therapeutic Screening Using Signaturities of INVENTION: Sets
FILE REFERENCE: 689230-69
FILE REFERENCE: 689230-69
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237,598
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 318
SOFTWARE: PatentIn version 3.0
SEQ ID NO 299
LENGTH: 383
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382 ATGCTGTCCAGACTGTCCGCTGTGTAAAAATAGGAATAAAGGGGGGGTTGTTATTTTT 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 CTGTCATCAGACAGGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGA 175
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1.8;
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Fatent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFRENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 ATAAAGGGGGTTGTTATTTTTACTGATATGTAAAATATAATTTGTA 224
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Pred. No. 1.8;
0; Mismatches 46; Indels
                                                                                     Indels
                                                     200 ACTGATATGTAAAATATAATTTGTATAAGAAAATGAGAGGGAGGGA
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1061
LENGTH: 309
                                                                                                                                                                                                                                                       Sequence 299, Application US/09969347 Patent No. US20020115085A1
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US-09-974-300-1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
; OTHER INFORMATION: n=a,t,g or c
US-09-969-347-299
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57.8%;
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Best Local Similarity 57.8°
Matches 63; Conservative
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Matches 57; Conservative
                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
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ORGANISM: Homo sapiens
                                                                                                                                                                                               RESULT 5
US-09-969-347-299/c
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US-09-974-300-1061
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APPLICATION NUMBER: 60/058,661
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APPLICATION NUMBER: 6
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DATE: 1997-07-08
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; OTHER INFORMATION: n equals a,t,g, or
US-09-983-802-133
                                                                                      PRIOR FILING DATE: EARLIER FILING DAPRIOR FILING DATE: EARLIER FILING DATE: EARLIER FILING DATE: EARLIER FILING DAPRIOR FILING DAPRIOR FILING DATE: EARLIER FILING DAPRIOR FILING DAPRIOR FILING DATE: EARLIER FILING DAPPING FILING DATE: EARLIER FIL
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2; Conservative
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LOCATION: (881)
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Matches 6
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GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 6942010
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR PELING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
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Pred. No. 17
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CURRENY APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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                                                                         Sequence 270, Application US/09954456 Patent No. US20020115057A1
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56.9%;
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Best Local Similarity
Matches 62; Conserv
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US-09-864-761-7942
RESULT 9
US-09-954-456-270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: HOMC
US-09-954-456-270
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Sequence 451, Application US/09834975
Sequence 451, Application US/09834975
Patent No. US20020110815a1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Bord, Andrew
APPLICANT: Wan Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, OF HUMAN CANCERS
FILE REPERENCE: MR. Of HUMAN CANCERS
FILE REPERENCE: MR. 106B
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILLING DATE: 2000-04-13
PRIOR FILLING DATE: 2000-04-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99004 GACTAACAGAAGGAATAGAATTAGTTTTTTTTTGCTAATTCAGTAATAGAACAAGTCATAT 98945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 TATGCTGTCCAGACTGTCCGCTGTGTAAAAATAGGAATAAAGGGGGGGTTGTTATTATTT 198
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 640681;
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             APPLICANT: SAKKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 TACTGATATGTAAAATATATTGTATAAGAAAATGAGA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.3%; Score 33; DB 10;
ilarity 50.7%; Pred. No. 11;
Conservative 0; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33.4; 1
Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 1046
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)...(425)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                              13.4%;
Similarity 47.0%;
APPLICANT: HATTORI, MASAHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Buchnera sp
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Best Local Similarity
                                                                                                                                                                                                                                                                                           LENGTH: 640681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-09-834-975-451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-834-975-451
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SEQ ID NO 451
LENGTH: 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 103;
                                                                                                                                                                                                                                                                                                                                                                      US-09-790-988-1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Best Local Similarity 49.7%; Pred. No. 9.1;
Matches 85; Conservative 0; Mismatches 86; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 GGGGTTGTTATTTTACTGATATGTAAATATAATTTGTATAAGAAAT 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
EXPRESSED IN PLACENTA, SIGNAL = 1.6
EXPRESSED IN HEART, SIGNAL = 1.5
EXPRESSED IN FETAL LIVER, SIGNAL = 0.99
EXPRESSED IN RETAIN, SIGNAL = 1.4
EXPRESSED IN BONE MARROW, SIGNAL = 1.2
EXPRESSED IN LUNG, SIGNAL = 1.2
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 7942
        OR FILING DATE: 2000-08-03

OR APPLICATION NUMBER: GB 24263.6

OR APPLICATION NUMBER: GB 24263.6

OR APPLICATION NUMBER: US 60/236,359

OR FILING DATE: 2000-09-27

OR APPLICATION NUMBER: PCT/US01/00665

OR APPLICATION NUMBER: PCT/US01/00665

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00669

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00669

OR APPLICATION NUMBER: PCT/US01/00665

OR APPLICATION NUMBER: PCT/US01/00665

OR APPLICATION NUMBER: PCT/US01/00665

OR APPLICATION NUMBER: PCT/US01/00665
                                                             PRIOR FELLING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PELLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PELLING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-21
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APPLICATION NUMBER: PCT/USO1/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00661
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00670
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Patent No. US20020127687A1
GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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                                   113 TGTCTGTCATCAGACAGGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAATA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 TGTCTGTCATCAGACAGGGTATTTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAATA 172
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                                                                                                                                                                                             Sequence 1458, Application US/09764868

Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: NUCLeic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT ETLING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1458
LENGTH: 2405
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TITLE DO INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT22
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1459
LENGTH: 3082
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                                                                        161 GTGTAAAAATAGGAATAAAGGGGGGTT 188
                                                                                             210 TTAAAAAAAAAAAAAAAGGGGGTTTT 237
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; Patent No. US20020168711A1
; GENERAL INFORMATION:
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55.2%;
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Best Local Similarity 55.2%;
Matches 64; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 55.23
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1459
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US-09-764-868-1459
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ENCOD
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APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Mandar, Min
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT E
TITLE OF INVENTION: NPOTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REPERENCE: 31133B
FILE OF INVENTION: NUMBER: US/10/108,605
CURRENT APPLICATION NUMBER: US 09/761,142
PRIOR APPLICATION NUMBER: US 60/761,142
PRIOR APPLICATION NUMBER: US 60/761,148
PRIOR FILING DATE: 2000-01-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3332 TGTTTAGAAATTAATAGAAAAAAAAAATGATTTGTATTCTAGAGATATATTATAATATTCT 3391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3212 TTGCCGGCAAGTGTAGGTGGGTGTTGTCTGCTGAGTGCATCCGCAACATCTATAGATAAT 3271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 GCTGTCCAGACTGTCCGCTGTGTAAAAATAGGAATAAAGGGGGGGTTGTTATTTTAC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 TGGCTGAAAACATTGAGCCTTTGATGACTGATTTGGCTGAAGAAGTGGATCGATTGT 81
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Best Local Similarity 47.2%; Pred. No. 29;
Matches 100; Conservative 0; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 TGATATGTAAAATATAATTTGTATAAGAAAT 233
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                             Sequence 254, Application US/10108605
Patent No. US20020160934A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-108-605-254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 361
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 254
LENGTH: 9224
                                                                                                                       APPLICANT: Broadus, Julie
                                                                                       GENERAL INFORMATION:
US-10-108-605-254
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AW292419 UI-H-BI2-AW001963 wt82d01.x BQ000230 UI-H-DI0-

AI989386 wt80e12.x AI697642 we15g02.x AI479617 tm32b12.x

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Shoo, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
Other_GSSs: CH230-5L12.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                   CH230-5L12.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-5L12, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhaoetigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                             CNS0000D1
BM153720
BM53720
CNS00FUH
AL789564
BE147799
C19410
AZ672806
BE110553
AZ672806
BR110553
AZ672806
AZ14029
CNS007ZY
CNS007ZY
CNS007ZY
CNS007ZY
CNS007ZY
CNS007ZY
AZ668475
                                                      CNS0182P
BH296588
BH279205
CNS01TL7
                                                                                                                                                                                                                                                                                       CNS01412
AV733775
CNS02D7F
                                                                                              AL527549
CNS017PG
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                                                                                               AL527
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1101
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BH362752
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BH362752/c
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DEFINITION
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KEYWORDS
SOURCE
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BE579975 kq35c02.y
AZ684739 ENTWR89TR
BH158622 ENTSV33TF
AQ266710 RPCIII-69
BE580320 kq39h02.y
                                                    ; Search time 1483 Seconds
(without alignments)
2719.269 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                       249
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                                                                                    US-09-936-145-1
249
1 gcccgcacatacgaaaaga.....aaatgagaggagatcc
                                                                                                                                                             32308132
      GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                            16154066 seqs, 8097743376 residues
                                                                                                                                                           Total number of hits satisfying chosen parameters:
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                                                     07:11:11
                                                                                                                                                                                                                      summaries
                                       using sw model
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BE579975
AZ684739
BH158622
AQ266710
BE580320
                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 su
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                                                     February 21, 2003,
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length: 2000000000
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gb_est4:*
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em_gss_rod:*
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                                     nucleic search,
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GSS 03-DEC-2001

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Result

AL108811 Drosophin BH295688 CH230-123 BH279205 CH230-24G AL166660 Tetracodon AL057308 Drosophin AL527549 AL527549 AL527549 AL527549 AL53720 TCBAP2E12 AA550133 1235m3 gm AL071063 Drosophin BM153720 TCBAP2E12 AA550133 1235m3 gm AL071063 Drosophin BL3720 TCBAP2E12 AL3729 RCI-HT022 CL9410 CL9410 Rice AZ691916 ENTGAL9TR BE110553 7n33401.x AL108712 Drosophin AL28167 Clone BAO AL108712 Drosophin BF632182 NF029A01D AL267280 Drosophin BF632182 NF029A01D AL267287 Drosophin BF632182 NF029A01D AL267347 BRTHEFTYR AL106774 TETRACOGON AL103568 Drosophin AL103568 Drosophin

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AZ684739/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE579975 549 bp mRNA linear EST 09-MAY-2001 kq35c02.yl TBN95TM-SSR Strongyloides stercoralis cDNA 5' similar to WP:ZC247.1 CE19306 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 549)
McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
Glibons,M., Ritter,E., Bannett,J., Franklin,C., Tsagareishvili,R.,
Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
Shin,T., Jackson,Y., Cardenas,M., McCann,R., Materston,R. and
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
The library was constructed by Dr. Thomas Nutman and colleagues of
                                                                                                                                                                                                                                                                                                        /sex="Female"
/cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by Pieter de Jong"
1 106 c 126 g 232 t
                                        (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plate: 5 row: L column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 AAAGAAGAACCATAAAAATACCTTGTCTGTCATCAGACAGGGTATTTTTATGCTGTC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 CAAAGTCTAAACAGAATCTATTACAGTAATGAATTAGGTAATCACAAAATTATATTCAAAA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 CAGACTGTCCGCTGTGAAAAAAAAAAAAAAAAAGGGGGGTTGTTATTATTTACTGATAT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strongyloides stercoralis.
Strongyloides stercoralis
Eukaryote, Metazoa, Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Strongyloides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 17; Length 668;
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Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98;
                                                                                                                                                                                                                   /strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="cH230-5112"
/clone_lib="CHORI-230 Segment 1"
                                                                                                                                                                                              /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.9%; Score 42.2; 50.8%; Pred. No. 2.
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BE579975.1 GI:9830917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 101; Conservative
                                                                                                                                                                            .668
                                                                                                           Seq primer: T7
Class: BAC ends
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BE579975
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/clone_lib=raxOH:02400
/lab_host="XL-1 Blue MRF" (Stratagene)"
/note="vector: Lambda Uni-2AP Rs (Stratagene); Site_1:
/note="vector: Lambda Uni-2AP Rs (Stratagene); Site_1:
ECORI: Site_2: XhoI: mRNA was purified from 2 x 10E3
rhabditiform larvae which had been isolated from gerbils
experimentally infected with larvae originally isolated
from experimentally infected dogs. CDNA was constructed
and, using adaptors, was cloned unidirectionally into the
vector from the EcoRI site to the XhoI site. The library
has an unamplified titer of 1 x 10E5 pfu/ml and an
amplified, undiluted titer of 9 x 10E11 pfu/ml. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ684739 846 bp DNA linear GSS 14-DEC-2000
ENTMP89TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: bjloftus@tigr.org Clones are derived from the Entamoeba histolytica \mbox{HM}\xspace:\mbox{Email}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281 ATAAACTTGTTGAAAAGGATGAACCATTAAAGACTGTTGATAATGATAAACAGGAAGAAA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                          /organism="Strongyloides stercoralis"
/strain="Rhabditiform larvae obtained from gerbils"
/db_xref="taxon:6248"
NIAID, NIH (tnutman@nih.gov). DNA Sequencing by: Washington University Genome Sequencing Center St. Louis.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 549;
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1 (bases 1 to 846)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences
HMI:IMSS sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.5%; Score 41.2; DI
56.7%; Pred. No. 4.2;
iive 0; Mismatches
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                                                          High quality sequence stop: 429.
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High quality sequence stop: 831.
Location/Qualifiers
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68 c 95 g
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Contact: Brendan J Loftus
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AZ684739
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AQ266710
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/db_xref="tar.ing."
/db_xref="tar.ing."
/db_xref="tar.ing."
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Vector: pHOS1; Site_1: BSt !; Constructed at The
Institute for Genomic Research (TIGR). Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a.
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENTSV33TF Entamoeba histolytica Sheared DNA Thear GSS 24-SEP-2001 genomic, DNA sequence.
BH158622
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The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
7213 301 838 0208
Fax: 301 838 3543
Elamil: bloftusetigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
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/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loftus, B., Wang, Z., Van Aken, S. and Fraser, C. Determination of clone end sequences from Entamoeba histolytica HM: IMSS sheared DNA library (2001) Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 GAAAAGAAGAAGACCATAAAAATACCTTGTCTGTCATCAGACAGGGTATTTTTTATGCTG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       657 TAACCAAAGAAAACCAACAGATATTGTTGTTTATACTGACTCATTTTGTTTTTCTGGGTG 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.5%; Score 41.2; DB 17; Length 846; 52.3%; Pred. No. 4.1; ive 0; Mismatches 83; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Entamoeba histolytica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 924)
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High quality sequence stop: 851.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="HM1:IMSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH158622.1 GI:15732060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 91; Conservative
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KEYWORDS
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SOURCE

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Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoneah histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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RPCII1-69D2.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-69D2, DNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 486)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, B., Wible, C., de Jong, P. and Venter, J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
Other_GSSS: RPCII1-69D2.TK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 GAAAAGAAGAACATAAAAATACCTTGTCTGTCATCAGACAGGGTATTTTTATGCTG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 TGAAAACATTGAGCCTTTGATGACTGATTTGGCTGAAGAAGTGGATCGATTGTTTGA 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.5%; Score 41.2; DB 17; Length 924; llarity 52.3%; Pred. No. 4.1; Conservative 0; Mismatches 83; Indels 0.
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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/db_xref="GDB:7526185"
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/clone_lib="RPCI-11"
/sex="Male"
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AQ266710.1 GI:3794314
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AUTHORS
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McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
Glbbons,M., Ritter,E., Bennett,J., Franklin,C., Tasqareishvili,R.,
Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
The library was constructed by Dr. Thomas Nutman and colleagues of
NaID, WIH (frutman@mih.gov). DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
High quality sequence stop: 421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             experimentally infected with larvae originally isolated from experimentally infected dogs. CDNA was constructed and, using adaptors, was cloned unidirectionally into the vector from the Bookl site to the Xhoi site. The library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="XL-1 Blue MRF' (Stratagene)"
/note="Vector: Lambda Unl-ZAP XR (Stratagene); Site_1:
EcoRI; Site_2: XhoI; mRM was purified from 2 x 10E3
rhabditiform larvae which had been isolated from gerblis
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library" 67 c 73 g 207 t
                                                                                                                                                                                                                                                                                                  CATAAAAATACCTTGTCTGTCATCAGACAGGGTATTTTTTATGCTGTCCAGACTGTCCGC 159
                                                                                                                                                                                                                                                                                                                                             76 TATATAATTITCCTTATTITGTACTGTCTTTGTAATTTTTTTAATATTAAGGCTATATGA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                      136 TCTCAGCAAATAAATACATTTCTTTTATGTTTATTTCCTTTCTTAAACACACAATAAAT 195
                                                                                                                                                                  Gaps
                                                                                                                                                                                                          40 CTTTGATGACTGATGATTTGGCTGAAGAAGAGGGATCGATTGTTTGAGAAAAGAAGAAGAC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Strongyloides stercoralis"
/Strain="Rabditificorm larvae obtained from gerbils"
/db_xref="taxon:6248"
/clone_lib="TBN95TM-SSR"
                                                                                                                                                                                                                                                       160 TGTGTAAAAATAGGAATAAAGGGGGGTTGTTATTATTTTACTGATATGTAAAATATAAT
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strongyloides stercoralis.
Strongyloides stercoralis
Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Strongyloides.
                                                                                                                  Length 486;
                                                                                                                                       Pred. No. 4.8;
0; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
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                                                                                                                    DB 17;
                                                                                                                       Score 41;
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                                                                                                                  16.5%;
49.8%;
                                                                                                                                       Best_Local Similarity 49.8
Matches 104; Conservative
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                                                                                                                    Query Match
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ORIGIN
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ORGANISM
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COMMENT
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BE580320
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Submitted (23-JuL-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European brosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS 26-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
has an unamplified titer of 1 x 10E5 pfu/ml and an amplified, undiluted titer of 9 x 10E11 pfu/ml. The average insert size of the unamplifed library is 675 bp (range, 100-1700)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genome survey sequence SP6 end of BAC BACA BACA FILO of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1099 KDDDWKDDTDRTWTDKKRKKKTTWKTADKKWTRWDTKDGGGGGGGGGGKGKKGKGGDRKADTK 1040
                                                                                                                                                                                                                                                                                                                     76 GATTGTTTGAGAAAAGAAGACCATAAAAATACCTTGTCATCAGACAGGGTATT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                           469 TATTGGTTGAANAAGGAAAACACCTCGAAGATGACATTTTTGGCATATTTAAAAGAGATT 528
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                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                              16 AAAGACTGGCTGAAAACATTGAGCCTTTGATGACTGATGATTTGGCTGAAGAAGTGGATC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                           Length 575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 others
                                                                                                                                                                                                                                          61; Indels
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Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74;
                                                                                                                                                                                              DB 10;
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                                                                                                                                                                                           Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1101 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /plasmid="pBeloBAC11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="DrosBAC"
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84 c 159 g
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Drosophila melanogaster
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                                                                                                                                                                                           Query Match
Best Local Similarity 55.8%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           529 TATCAGATTATCCAAAAT 546
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TAG_SEQ=CAAC"
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1 Similarity 73.5%;
50; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 AAGAAAAT 260
                                                                                                                                                                                                                                                                                                                                                                                                                              107
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AW001963
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//db_xxef="taxon:960es"
/clone=lib="NoI_CGAP_Sub4"
/clone=lib="NoI_CGAP_Sub4"
/lab_host="bH10B (Life Technologies)"
/lab_host="bH10B (Life Technologies)"
/note="Vector: p773D-Pac (Pharmacia) with a modified
/note="Vector: p773D-Pac (Pharmacia) with a constitutes a
mixture of 21 normalized or subtracted NGLCGAP
Ilbraries: NGLCGAP_Cod, NGLCGAP_Exid)
/NGLCGAP_LOG, NGLCGAP_Exid)
/NGLCGAP_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapDs-remail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand CDNA and therefore this may represent a bonafide poly A tail. CDNA Library Preparation: M. B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 16-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI_CGAP_Kid3 pool | : LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-145677, 1500552-1502855) NCI_CGAP_Kid5 pool | : LLAM 3388-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs 132912-1325831, 1471368-1472903, 1492104-1493255) NCI_CGAP_Lub pool | : LLAM 3575-3782, 376-378 (IMAGE CloneIDs 1414220-1417991, 1520904-1522439) NCI_CGAP_GC4 pool | : LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW292419
392 bp mRNA linear EST 16-JAN-2
UI-H-BIZ-agw-h-08-0-UI.S1 NCI_CGAP_Sub4 Homo sapiens cDNA clone
IMAGE:2725886 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T.M.A.G.E. Consortiun/LDLNL at:
www-bio.llnl.gov/bbrp/image/image.html The following repetitive
elements were found in this cDNA sequence: 1-30,
>AT_richtLow_complexity
Seq primer: Mi3 Fourard
1039 RDWRGAATRRARWATAATTATADDTWKRTTGTKTRTWKWKWWARRAAKWRDWWRDTDWWD 980
                                                                    201 CTGATATGTAAAATATATTTGTATAAGAAAATGAGAGGAGA 243
                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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AW292419
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KEYWORDS
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FEATURES

TITLE

SOURCE

COMMENT

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NCI_CGAP_Pr22 pool 1: LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS 985608-986759, 1101192-1101959, 127928-1220615) NCI_CGAP_CO10 pool 1: LLAM 2644-2653, 2871-2872 (IMAGE CloneIDS 1057416-1061255, 1144584-1145351) Subtraction was performed as previously described [Bonaddo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.]
TAG_LIS-NCI_CGAP_Lu5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 461)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbos-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 696 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 448.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 AAAAATAGGAATAAAGGGGGGTTGTTATTTTTTACTGATATGTAAAATATATTTGTAT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW001963 461 bp mRNA linear EST wt82d01.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2513953 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39.2; DI
Pred. No. 13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                            113 g
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9

0;

0; Gaps

EST 08-SEP-1999

Query Match Best Local Matches 5

Оp ò g RESULT 10 BQ000230/c DEFINITION

ORGANISM

SOURCE

AUTHORS

TITLE

JOURNAL

COMMENT

REFERENCE

ACCESSION

VERSION KEYWORDS

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AI697642 475 bp mRNA linear EST 18-DEC-1999 we15902.xl NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2341202 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpoublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.nih.gov
Email: cgapbs.r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 442.
                                                166 AAAAATAGGAATAAAGGGGGTTGTTATTATTTTACTGATATGTAAAATATAATTTGTAT 225
                                                                         166 AAAAATAGGAATAAAGGGGGGTTGTTATTTTTACTGATATGTAAAATATAATTTGTAT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Eco RI sites of the modified pT7T3 vector. Lik went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                          A1989386 467 bp mRNA linear EST vt80e12.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2513806 3', mRNA sequence.
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    Indels
  18;
  Mismatches
  0;
                                                                                                                                                                                                                                                                                                                                                                                                         AI989386.1 GI:5836309
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Best Local Similarity 73.5%;
Matches 50; Conservative (
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                    wt80e12.x1
                                                                                                                                             AAGAAAAT 233
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DEFINITION
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ORIGIN
                                                                                                                                                                                         210
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    Matches
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AI697642
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                                                                                                                                                                                                                                                              RESULT 11
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                 BOO00230
UI-H-DIO-avp-j-04-0-UI.sl NCI_CGAP_DIO Homo sapiens cDNA clone
IMAGE:5882595 3', mRNA sequence.
                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov

Issue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

rhe following repetitive elements were found in this cDNA

sequence: 433 454, >AT_ich#Low_complexity (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Bouble stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (TI) at a library is contained to be sequenced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_1: EGOR 1; Site_2: Not I; NCI CGAP DIO is a CDNA library containing the following tissue(s): A pool of Lung Focal Fibrosis. The library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 462)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap..
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                     166 AAAAATAGGAATAAAGGGGGGTTGTTATTTTTACTGATATGTAAAATATATTTGTAT 225
                                                0;
    Length 461;
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                                                Indels
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/tissue_type="Lung Focal Fibrosis"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
  DB 10;
                                                18;
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                                              0; Mismatches
                          Pred. No. 13;
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Pred. No. 13;
15.7%; Score 39.2; 73.5%; Pred. No. 13
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/db_xref="taxon:9606"
/clone="IMAGE:5882595"
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73.5%;
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Unpublished (1997)
                                              50; Conservative
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                        Similarity
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                                                                                                                                                                                                                                   236 AAGAAAAT 243
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source

FEATURES

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Query Match

BASE COUNT

Library

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Conservative
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      Tumor Gene Index
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VERSION
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SOURCE
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                                      COMMENT
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                                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_LuS was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 144920-1417991 and 152094-1552439). Subtraction by Bento
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                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 564)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                 1 (bases 1 to 475)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 AAAAATAGGAATAAAGGGGGGTTGTTATTTTTACTGATATGTAAATATATTTGTAT 225
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                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 701 Std Error: 0.00
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109 c 130 g 89 t
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Pred. No. 13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:2341202"
/clone_lib="NCI_CGAP_Lu24"
                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="carcinoid"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -400P from Gibco
High quality sequence stop: 465.
Location/Qualifiers
AI697642
AI697642.1 GI:4985542
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Matches 50; Conservative
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                                                            human.
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AUTHORS
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TITLE
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Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNSO182P 1101 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37D10 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) + http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 AAAAATAGGAATAAAGGGGGGTTGTTATTTTTACTGATATGTAAAATATATTTTGTAT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/clone="IMAGE:2158271"
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/tissue_Lype="B-cell, chronic lymphotic leukemia"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                 www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 685 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.7%; Score 39.2; 73.5%; Pred. No. 13
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fly), genomic survey sequence.
AL108811
AL108811.1 GI:5629115
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                        Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
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BASE COUNT
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S 2hao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn

A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de
Jong, P. and Fraser, C.M.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment

Unpublished (1999)

Other_GSSs: CH230-123115.TVB

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ore ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ering_information.htm). BAC end
Plater: 123 row: I column: 15
Seg primer: SP6
Class: BAC ends.
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0
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project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CH230-123115.TJB CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-123115, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                      87 AAAAGAAGAACCATAAAAATACCTTGTCTGTCATCAGACAGGGTATTTTTATGCTGT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 CCAGACTGTCCGCTGTGTAAAAATAGGAATAAAGGGGGGGTTGTTATTATTTTACTGATA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                              27 GAAAACATTGAGCCTTTGATGACTGATGATTTGGCTGAAGAAGTGGATCGATTGTTTGAG 86
                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                              15.5%; Score 38.6; DB 17; Length 1101; 15.7%; Pred. No. 18;
                                                                                                                                                                                                                                   358 others
                                                                                                                                                                                                                                                                                                                                       75; Indels
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/db_xref="taxon:7227"
/clone="BACN37D10"
/clone="lorosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
*a 268 c 128 g 73 t 358 ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::|: ::::::| |::::::| |::::|| |::::|| 996 DKTWTRDWWWWTRTKWDWWWDDGRGRGRGRWTRKRWGA 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 TGTAAAATATATTTGTATAAGAAAATGAGGGGGGA 243
                                                                                                                                                                                                                                                                                                                                       34; Conservative 108; Mismatches
                                                             Location/Qualifiers
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                                         pBeloBAC11
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BH296588/c
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
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source

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ö
/strain="BN/Sachsd/MCW"
/db_xref="taxon:10116"
/clone="cH230-123115"
/clone_lib="cH0R1-230 Segment 1"
/sex="Female"
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CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          764 GAAAAAAATGATTTTTTTTAAATATTGAAATGGTTAAAGATTTTGGGGAAATCCAAAAG 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 AAAAGAAGAAGACCATAAAAATACCTTGTCTGTCATCAGACAGGGTATTTTTATGCTGT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    704 TCAGGAATAAAATGAAAGAATTCACTGGTGCATCAAGAAAAAGGAAATTCTCCATAGAAA 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 CCAGACTGTCCGCTGTGTAAAAAATAGGAATAAAGGGGGGGTTGTTATTATTTTACTGATA 206
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 GAAAACATTGAGCCTTTGATGACTGATTTTGGCTGAAGAAGTGGATCGATTGTTTGAG 86
                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                            Length 784;
                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                         Query Match 15.4%; Score 38.4; DB 17; Best Local Similarity 49.5%; Pred. No. 20; Matches 99; Conservative 0; Mismatches 101;
                                                                                                                                                                                                                                                         349 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: February 21, 2003, 08:05:17 Job time : 1492 secs
                                                                                                                                                                                                                                                         ĭ18 g
                                                                                                                                                                                                                               Pieter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 TGTAAAATATATTTGTATA 226
                                                                                                                                                                                                                                                         133 c
                                                                                                                                                                                                                                                            184
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

February 21, 2003, 07:16:20 ; Search time 76 Seconds Run on:

(without alignments) 1004.770 Million cell updates/sec

US-09-936-145-1

249

1 gccccgcacatacgaaaaga.....aaatgagagagagatcc Perfect score: Sequence:

Scoring table:

441362 seqs, 153338381 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Issued_Patents_NA:*

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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ф			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
П	246	98.8	2604	4	US-09-264-097-3	Sequence 3, Appli
7	246	98.8	2604	4	US-09-537-168-5	5
ю	242.8	97.5	2084	-	US-08-720-899-3	'n
4	242.8	97.5	2084	Н	US-08-459-610-3	'n
S	242.8	97.5	2084	7	US-08-343-804-3	'n
9	242.8	97.5	2084	7	US-08-687-399-3	'n
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80	242.8	97.5	2084	က	US-08-683-838A-3	ω,
σ	242.8	97.5	2084	m	US-09-182-859-3	Sequence 3, Appli
10	242.8	97.5	2084	4	US-09-170-670-13	13,
11	242.8	97.5	2084	4	US-09-193-068-31	31,
12	242.8	97.5	2084	4	US-09-183-412-58	58,
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16	170.8	9.89	10216	7	US-08-875-154-1	Sequence 1, Appli
17	162	65.1	185	4	US-09-384-305-20	20,
18	162	65.1	185	4	US-09-258-377-25	25,
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20	158.8	63.8	162	-	US-08-459-967-24	24,
21	158.8	63.8	162	П	-08-460-327-	24,
22	158.8	63.8	162	П	871-	24,
23	157.2	63.1	185	4	-09-384-	22,
24	157.2	63.1	185	4	-09-258-377-	27,
25	155.6	62.5	185	4	-09-384-	21,
56	155.6	\sim	185	4	-60-	
27	39.5	15.7	44	4	US-09-384-305-15	15,

88, 88, 84, 86, 84, 84, 84, 84, 84, 84, 84, 84, 84, 84	Sequence 18, Appl Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl	Sequence 26, Appl Sequence 38, Appl Sequence 10, Appl Sequence 26, Appl	Seguence 10, Appl Seguence 133, App Seguence 1, Appli
US-09-258-377-19 US-07-991-8678-8 US-08-107-755A-8 US-08-544-332-8 US-09-370-861A-8 US-08-392-625-16 US-08-466-961A-16	US-08-645-193B-18 US-08-434-255-26 US-08-459-967-26 US-08-460-327-26	US-08-459-871-26 US-08-873-479-38 US-09-031-442A-10 US-08-972-661A-26	US-09-258-377-10 US-09-227-357-133 US-09-251-645-1
4110400	2444	H 2 2 2	444
44 1511 1511 1511 1511 1511 8700 8700	8700 34 34 34	4 4 4 4 4 8 8 8 8	43 882 9717
15.7 14.6 14.6 14.6 14.2	14.2 13.7 13.7 13.7	13.7 13.7 13.7 13.7	13.7 13.6 13.4
3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	35.4 34 34 34	3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	33.8 33.4
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                 1 GCCCGGCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTGATGACTGATGATTTGG 60
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                                  GENERAL INFORMATION:
APPLICANT: NO. 6287826man, Barrie Edmund
APPLICANT: Hendriksen, Hanne Vang
ITILE OF INVENTION: Enzymatic Preparation of Glucose Syrup
TITLE OF INVENTION: From Starch
FILE REFERENCE: 5278.200-US
CURRENT APPLICATION NUMBER: US/09/264,097
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: PA 0321/98
EARLIER FILING DATE: 1998-03-09
EARLIER FILING DATE: 1998-03-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 2604
                                                                                                                                                                                                                                                                                                                                                       Length 2604;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                     98.8%; Score 246; DB 4; 100.0%; Pred. No. 1.9e-59; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                           TYPE: DNA
; ORGANISM: Bacillus amyloliquefaciens
US-09-264-097-3
                           Sequence 3, Application US/09264097
Patent No. 6287826
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.C
Matches 246; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAGGA 246
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AGAGGA 766
RESULT 1
US-09-264-097-3
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RESULT 2

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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: LOWNEY DI., KAREN A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,899
FILING DATE: 10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 3, Application US/08459610
; Patent No. 5801043
                                                                                                                                                                                                                                                 TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.2%;
                                                                                                                                                                                                                                                                                                     LENGTH: 2084 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                      CLASSIFICATION:
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LOCATION:
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FEATURE:
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CITY: Ne
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                                                              APPLICANT: Andersen, Carsten
APPLICANT: Andersen, Christel T.
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Kjaerulff, Soren
TITLE OF INVENTION: Alpha-Amylase Variants
FILE REFERENCE: 5886.200-US
CURRENT APPLICATION NUMBER: US/09/537,168
CURRENT FILING DATE: 1909-03-29
EARLIER APPLICATION NUMBER: PA 1999 00437
EARLIER APPLICATION NUMBER: 60/127,427
EARLIER APPLICATION NUMBER: 60/127,427
EARLIER FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 40
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Prec. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bisgaard-Frantzen, Henrik APPLICANT: Borchert, Torben Vedel APPLICANT: Svendsen, Allan APPLICANT: Thellersen, Marianne APPLICANT: Van der Zee, Pia TITLE OF INVENTION: AMYLASE VARIANTS
                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
            Sequence 5, Application US/09537168 Patent No. 6410295 GENERAL INFORMATION:
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Patent No. 5753460
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Matches 246; Conservative
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CITY: New York
STATE: New York
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LENGTH: 2604
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US-09-537-168-5
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US-08-720-899-3
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APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58010430 No. 5801043disk of No. 5801043th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor Gaps 1 GCCCCGCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTGATGACTGATGATTTGG 60 ö Length 2084; Indels Score 242.8; DB 1 Pred. No. 1.3e-58;

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E: No. 58308370 No. 5830837disk of No. 5830837th America, Inc. 405 Lexington Avenue, 64th Floor
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                                                                                                                           COUNTRY: USA
ZIP: 10174-6401.
COMPUTER READABLE FORM:
MEDLUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-FOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.5%; Score 242.8; DB 2; 99.2%; Pred. No. 1.3e-58;
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                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/343,804
FILING DATE: 22-NOV-1994
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2084 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 244; Conservative
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343..1791
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250..342
                                                  CORRESPONDENCE ADDRESS:
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                                                                                               New York
New York
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                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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LOCATION:
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                                                                                STREET:
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                                                                         COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,610
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                     NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-US
TELECOMMUNICATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bisgaard-Frantzen, Henrik
Borchert, Torben Vedel
Svendsen, Allan
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Patent No. 5830837
GENERAL INFORMATION:
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2084 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                              ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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343..1791
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250..342
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 New York
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION:
US-08-459-610-3
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                  COUNTRY:
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Best Local S
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NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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250..342
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250..1791
                                                                                                                        TITLE OF INVENTION: '-NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                     CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 13 CLASSIFICATION:
                                                                                                                                                                     ADDRESSEE:
STREET: 40
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FEATURE:
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                JS-08-600-908A-3
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 RESULT 7
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                                                                                                                 E: No. 59283810 No. 5928381disk of No. 5928381th America, Inc. 405 Lexington Avenue, 64th Floor
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           APPLICANT: Marcher, Dorthe
APPLICANT: Pedersen, Hanne H.
APPLICANT: Nilsson, Thomas E.
APPLICANT: NILSSON, A Combined Desizing and Bleaching
TITLE OF INVENTION: Process
                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 242.8; DB 2;
Pred. No. 1.3e-58;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 008
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
RECISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4127.204-US
                                                                                                                                                                                  COUNTRY: United States of America ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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99.28;
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
Toft, Annette H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2084 base pairs
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343..1791
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250..342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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250..1791
                                                                                       NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                     CITY: New York
STATE: New York
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                                                                                                                      ADDRESSEE:
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LOCATION:
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LOCATION:
US-08-687-399-3
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FEATURE:
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AGAGGA 246

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99.2%; Pred. No. 1.3e-58;
tive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/600,908A
FILING DATE: 13-FEB-1996
                                                                                                                                                                                                                         405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4394.204-US
                                                            APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                            COUNTRY: United States of America ZIP: 10174-6401
Sequence 3, Application US/08600908A Patent No. 5989169
GENERAL INFORMATION:
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181 GGGGGGTTGTTATTTTACTGATATGTAAAATATAATTTGTATAAGAAATGAGAGGG 240
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Pred. No. 1.3e-58;
0; Mismatches 2;
                                                                                                                                                                                                                                      APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
TILE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204.0S
CURRENT APPLICATION WUMBER: US/09/182,859
CURRENT APPLICATION WUMBER: 0515/96
EARLIER APPLICATION WUMBER: 0712/96
EARLIER APPLICATION WUMBER: 0712/96
EARLIER APPLICATION WUMBER: 0775/96
EARLIER FILING DATE: 1996-06-28
EARLIER PILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-11-08
NUMBER OF SEO ID NOS: 37
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APPLICANT: Svendert, Torben
APPLICANT: Bisgard-Frantzen Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REPERENCE: 5276.200-US
CURRENT APPLICATION NUMBER: US/09/170,670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Bacillus amyloliquefaciens
US-09-182-859-3
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US-09-170-670-13
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Best Local
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                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,838A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 242.8; DB 3;
Pred. No. 1.3e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
PPLICATION NUMBER: US 08/600,908
FILING DATE: 13-FBB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-878-9655
                                                                                                                                TITLE OF INVENT: Borchert, Torben Vedel
TITLE OF INVENTION: 'Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO FACE.
                                                                                                                GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Erantzen, Henrik
APPLICANT: BORCChert, Torben Vedel
                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America ZIP: 10174-6401
                                                                                  ; Sequence 3, Application US/08683838A; Patent No. 6022724
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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250..342
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250..1791
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                                                                                                                                                                                                                                                                                             New York
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Best Local Similarity
                                                                                                                                                                                                                                                                         CITY: New York
241 AGAGGA 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
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LOCATION:
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; LOCATION:
US-08-683-838A-3
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121 ATCAGACAGGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAATAAGGAATAAA 180
                                               GGGGGGTTGTTATTATTTACTGATATGTAAAATATAATTTGTATAAGAAAATGAGAGGG
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; LOCATION: (343)...(1794)
US-09-183-412-58
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AGAGGA 246
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SEQ ID NO 58
LENGTH: 2084
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US-09-183-412-58
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US-09-290-734-13
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Pred. No. 1.3e-58;
                                                                                                                                                                                       DB 4;
                                                                                                                                                                                    Query Match 97.5%; Score 242.8; DB 4; Best Local Similarity 99.2%; Pred. No. 1.3e-58; Matches 244; Conservative 0; Mismatches 2;
CURRENT FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 1172/97
EARLIER FILING DATE: 1997-10-13
EARLIER FILING DATE: 1997-10-18
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SOGTWARE: 2084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/09193068
Patent No. 6197565
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Bisgaard Frantzen, Henrik
APPLICANT: Andersen, Carsten
TITLE OF INVENTION: -Amylase Variants
FILE REFERENCE: 5709.000-US
CURRENT APPLICATION NUMBER: US/09/193,068
CURRENT FILING DATE: 1998-11-16
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                           ; ORGANISM: B. amyloliquefaciens
US-09-170-670-13
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99.2%;
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Best Local Similarity 99.2
Matches 244; Conservative
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241 AGAGGA 246
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US-09-193-068-31
                                                                                                                                TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.5%; Score 242.8; DB 4 Best Local Similarity 99.2%; Pred. No. 1.3e-58; Matches 244; Conservative 0; Mismatches 2
                                                                                                 APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne.
APPLICANT: Nielsen, Bjarne.
APPLICANT: Nissen, Torben L.
APPLICANT: Nissen, 1050-03
CURRENT APPLICATION NUMBER: 60/064,662
EARLIER APPLICATION NUMBER: 60/093,234
EARLIER APPLICATION NUMBER: 60/093,234
EARLIER APPLICATION NUMBER: 1240/97
EARLIER APPLICATION NUMBER: 1240/97
EARLIER APPLICATION NUMBER: 1240/97
EARLIER APPLICATION NUMBER: 1998-07-17
EARLIER PELLING DATE: 1998-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Bacillus amyloliquefaciens
Sequence 58, Application US/09183412 Patent No. 6204223. GENERAL INFORMATION: APPLICANT: Borchert, Torben V.
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ORGANISM: Bacillus amyloliquefaciens
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                                                      97.5%;
99.2%;
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                                                                          Best_Local Similarity 99.2
Matches 244; Conservative
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NAME/KEY: CDS
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                US-09-672-459-3
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        GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Brigard-Francen Henrik
APPLICANT: Bisgard-Francen Henrik
APPLICANT: Outtrup, Helle
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Vibeke Skovgaard
TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mutants
FILE REPRENCE: 5276.400-US
CURRENT FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Borchert, Torben
APPLICANT: Bosgard-Frantzen, Henrik
TTLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/672,459
CURRENT FILING DATE: 1998-10.29
PRIOR PILING DATE: 1998-10.29
PRIOR PILING DATE: 1996-04-30
PRIOR PILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-07-11
PRIOR PILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 3, Application US/09672459
; Patent No. 6436888
                                                                                                                                                                                                                                                                                                                                            ORGANISM: B. amyloliquefaciens
US-09-290-734-13
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241 AGAGGA 246
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LENGTH: 2084
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Length 2084;
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                             Indels
Score 242.8; DB 4;
Pred. No. 1.3e-58;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/09/636,252A
CURRENT FILING DATE: 1996-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 16
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2084
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241 AGAGGA 246 ||||||| 241 AGAGGA 246

δy QQ

Search completed: February 21, 2003, 08:06:42 Job time: 80 secs

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February 21, 2003, 06:31:25; Search time 227 Seconds (without alignments) 2470.254 Million cell updates/sec
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2185239 seqs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                           - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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249
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Maximum DB s
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CIMMADIDG

SUMMAKLES		Description			AAZ21079 Bacillus amyloliqu						
กั		ID	AAA	AAA	AAZ	AAA	AAO:	AAN2	AAO	AAO	2 4 4
		DB	21	21	20	22	13	٣	16	16	20
		re Match Length DB]	249	270	2604	2604	537	576	2084	2084	7007
ď	Query	Match	100.0	100.0	98.8	98.8	97.5	97.5	97.5	97.5	7 7
		Score	249	249	246	246	242.8	242.8	242.8	242.8	0 676
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WPI; 2000-594327/56

Wild type Termamyl Bacillus amyloliqu Termamyl-like-alph B. amyloliquefacie Bacillus alpha amy Bacillus DNA encod Bacillus amyloliqu	C-terminal Subtili DNA construct A co Subtilisin 309-CI- DNA construct B co PamyL ATG-barley C DNA construct D co Transposon deliver B thuringiensis w	Bacillus amyloliqu Wild type amyO pro Bacillus sp. amyO Bacillus amyloliqu Banilus amyloliqu BAN promoter. Bac B. amyloliquefacie Bacillus amylolique Consensus amyQ pro B. amyloliquefacie Bacillus amylolique Consensus amyO pro Consensus amylolique	Plasmid pMOLI642. Nucleotide sequenc Sequence of the ar Oligo #2 used in t Bacillus amyloliqu Oligo #1 used in t amyQ promoter olig Human neuroblastom Human chemically m Human immune syste
AAX57596 AAA48484 ABL96211 ABL50568 AAT72215 AAS20026 AAV02472	AAD34433 ABL44434 AAL44434 AAD34436 AAD34436 AAT39279 AAZ33322	AAD09922 AAC62645 AAC93325 AAD09931 AAC33324 AAC62647 AAC62647 AAC6263323 AAC62646	AAD29902 AAH25109 AAN50418 AAD09917 AAZ23340 AAD09916 AAF62640 AAF62640 ABN80014 ABL32604
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97.5 97.5 97.5 97.5 97.5	688.6 688.6 67.6 67.3 67.3	00000000000000000000000000000000000000	43.0 38.9 18.6 16.2 15.7 15.7 15.7 15.7 15.3
242.8 242.8 242.8 242.8 242.8 242.8 242.8	170.8 170.8 170.8 170.8 170.8 167.6	162 162 160.4 158.8 157.2 157.2 157.2 1155.6 1155.6	100 100 100 100 100 100 100 100 100 100
10 11 11 13 14 15	17 19 20 23 23 24		888844444 97886 97864444444
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ALIGNMENTS

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Alpha-amylase promoter; restriction enzyme cleavage site; expression cassette; expression vector; recombinant protein production;
                                                                                                                                                                                                                                                                         Yamamoto Y, Ohshima Y;
                                                                             Bacillus amyloliquefaciens alpha-amylase promoter.
                                                                                                                                                                                                                                                                        Inoue Y, Fushimi N, Mizubuchi H,
Yasutake N, Miyoshi S;
                  AAA93677 standard; DNA; 249 BP.
                                                                                                                                                                                                  08-MAR-2000; 2000WO-JP01415.
                                                                                                                                                                                                                      99JP-0060904
99JP-0286034
                                                                                                                                     Bacillus amyloliquefaciens.
                                                          16-JAN-2001 (first entry)
                                                                                                                                                                                                                                                     (SHOS ) SHOWA SANGYO CO.
                                                                                                                                                           WO200053778-A1.
                                                                                                                                                                                                                      08-MAR-1999;
06-OCT-1999;
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                                      AAA93677;
RESULT 1
          AAA9367.
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(SHOS ) SHOWA SANGYO CO
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                                                                                                                                The invention relates to a modified Bacillus amyloliquefaciens alpha-amylase promoter (AAA93678) which has a higher activity than the wild-type alpha-amylase promoter (AAA93677). The modified promoter contains several restriction enzyme cleavage sites near the 3' end. The invention also encompasses an expression cassette comprising the novel promoter, an expression vector comprising the expression cassette, host cells transformed with the expression vector, and the preparation of a gene product using cells transformed with the expression vector. The modified promoter of the invention and constructs and host cells comprising it may be used for the recombinant production of proteins for use as pharmaceuticals or foodstuffs. The present sequence represents the wild-type Bacillus amyloliquefaciens alpha-amylase promoter used in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified alpha-amylase promoter; restriction enzyme cleavage site; expression cassette; expression vector; recombinant protein production; mutant; ds.
Modified Bacillus alpha-amylase promoter having additional restriction sites near the 3'-terminus for higher promotion of gene expression in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GGGGGGTTGTTATTTTACTGATATGTAAAATATATTTGTATAAGAAAATGAGAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 249; 100.0%; Pred. No. 8
                                                                                           Example 2; Page 39; 48pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA93678 standard; DNA; 270 BP.
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99JP-0286034
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Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-1999;
06-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-2000
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                                            Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA93678;
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This sequence represents a novel modified Bacillus amyloliquefaciens alpha-amylase promoter which has a higher activity than the wild-type alpha-amylase promoter (AAA93677). The modified promoter contains several restriction enzyme cleavage sites near the 3 end. The invention also encompasses an expression cassette comprising the novel promoter, an expression vector comprising the expression cassette, host cells transformed with the expression vector, and the preparation of a gene product using cells transformed with the expression vector. The modified promoter of the invention and constructs and host cells comprising it may be used for the recombinant production of proteins for use as pharmaceuticals or foodstuffs.
                                                                                                           Modified Bacillus alpha-amylase promoter having additional restriction sites near the 3'-terminus for higher promotion of gene expression in Bacillus .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGGGTTGTTATTATTACTGATATGTAAAATATATTTGTAAGAAAATGAGAGGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha-amylase; Termamyl-like alpha-amylase; glucose syrup; starch; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus amyloliquefaciens Termamyl-like alpha-amylase encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCCCCGCACATACGAAAAGACTGGCTGAAACATTGAGCCTTTGATGACTGATTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCCCCGCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTGATGACTGATTTGG
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  Ohshima Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 270 BP; 89 A; 40 C; 67 G; 74 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 249; DB 21;
; Pred. No. 8.2e-58;
0; Mismatches 0;
Mizubuchi H, Yamamoto Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 707..712
                                                                                                                                                                                                            Claim 7; Page 39; 48pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ21079 standard; DNA; 2604 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
100.0%;
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729..734
/*tag= b
759..762
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Best Local Similarity 100.
Matches 249; Conservative
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Fushimi N,
                   Miyoshi
                                                                 WPI; 2000-594327/56
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                     Tasutake N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-NOV-1999
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-10_signal
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Inoue Y,
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                                                                                                                                                                                                                                                                                             30-MAR-1999;
                                                                                                                                                                                                                                                                                                                                      Kjaerulff S;
                                                                                                                                                                    sig_peptide
                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                             12-OCT-2000
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                                                                         -10_signal
                                                                                          .35_signal
                                                                                                                                                                                                                     terminator
                                                                                                          RBS
                                                                                                                          CDS
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                                                                                                                                                                                                                                         A method has been developed for the preparation of a glucose syrup using a Termamyl-like alpha-amylase containing a substitution at Val(54). The glucose syrup obtained by the process is useful as an ingredient in food products. The Termamyl-like alpha-amylase facilitates the preparation of glucose syrups suitable for the food industry, previously only possible using acid hydrolysis. The present sequence encodes Bacillus amyloliquefaciens Termamyl-like alpha-amylase.
                                                                                                                                                                                                                                                                                                                                                                      ATCAGACAGGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGAATAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFCAGACAGGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGAATAAA 700
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                           Preparation of a glucose syrup, using a Termamyl-like alpha-amylase
                                                                                                                                                                                                                                                                                                                                                              GCCCCCCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTGATGACTGATTTGG
                                                                                                                                                                                                                                                                                                                                                                                                       GGGGGGTTGTTATTATTTACTGATATGTAAAATATATTTGTATAAGAAAATGAGAGGG
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                                                                                                                                                                                                                                                                                                                             Length 2604;
                                                                                                                                                                                                                                                                                                                                             Indels
                "Termamyl-like alpha-amylase"
                                                                                                                                                                                                                                                                                                             Sequence 2604 BP; 755 A; 516 C; 684 G; 649 T; 0 other;
                                                                                                                                                                                                                                                                                                                                             ·.
                                                                                                                                                                                                                                                                                                                           98.8%; Score 246; DB 20;
100.0%; Pred. No. 9.3e-57;
iive 0; Mismatches 0;
                                                                                                                                                                                                                           Disclosure; Page 29-32; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA37850 standard; DNA; 2604 BP.
                                                                                                                  99WO-DK00114
                                                                                                                                 98DK-0000321
                                                /*tag= f
2321..2376
/*tag= g
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863..2311
                                                                                                                                                                  Norman BE, Hendriksen HV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
              /product=
.2314
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Best Local Similarity 100.
Matches 246; Conservative
                        770..862
                                                                                                                                                 (NOVO ) NOVO-NORDISK AS.
        ′*tag=
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                                                                                                                08-MAR-1999;
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                                                                                                                                 09-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-FEB-2001
                        sig_peptide
                                        mat_peptide
                                                                                                 16-SEP-1999
                                                         terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA37850;
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This sequence encodes a termamyl-like alpha amylase.

The invention relates to a variant (I) of parent Termamyl-like
alpha-amylase comprising alteration at one or more of the positions
(I) 448, T49, S50, O51, A52, D53, V54, G107, G108, A11, S168 and
(I) GAR T49, S50, O51, A52, D53, V54, G107, G108, A11, S168 and
(II) The alterations in (I) are independently an insertion of an amino
acid which occupies the position or deletion
or substitution of the amino acid which occupies the position or deletion
or substitution of the amino acid which occupies the position with a
different amino acid. The variant has alpha-amylase activity. (I) or
compositions containing it are useful in starch liquefaction, in
certains compositions, ethanol production such as fuel, drinking and
industrial ethanol production, desizing of textiles, fabrics or garments.
(I) exhibits a reduced capability of cleaving a substrate close to the
branching point, and further exhibits improved substrate specificity
and/or improved specific activity relative to the parent alpha-amylase.
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Termamyl-like alpha-amylase; variant; starch liquefaction; fuel; detergent composition; laundry cleaning composition; ethanol production; dish washing cleaning composition; hard surface cleaning composition; industrial ethanol production; textile desizing; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= alpha-amylase
/note= "the signal peptide is not shown in the encoded
protein given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New variants of parent Termamyl-like alpha-amylase, useful in star
liquefaction, in detergent compositions and in ethanol production,
exhibit altered cleavage pattern relative to the parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "the signal peptide is not shown in specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 246; DB 22;
Pred. No. 9.3e-57;
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                                                                                                                                                                                                                       Location/Qualifiers 707..712
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100.0%; Pre
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/note= "the
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2321..2376
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                                                                                                                                                             Bacillus amyloliquefaciens
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759..762
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770..2314
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Best Local Similarity 100.
Matches 246; Conservative
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729..734
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Example; Fig 3; 51pp; English.
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AAN20046
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                           ATCAGACAGGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAATAGGAATAAA 180
                                                             240
                                                                                        Heterologous regulatory promoter module; hyperexpression; secretion; Bacillus expression system; RNA polymerase initiation site; ds.
       GCCCCGCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTGATGACTGATGATTTGG
                                                                                 GGGGGGTTGTTATTTTACTGATATGTAAAATATATTTGTATAAGAAAATGAGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hybrid alpha-amylase promoter for recombinant gene expression -
in prokaryote(s), esp. bacillus subtilis, contg. target module of
enhancer gene for ribonucleic acid
                                                                                                                                                                                               Sequence of the NH2 region of the B. subtilis alpha-amylase gene
                                                                                                                                                                                                                                                                                                                                   primer 303"
                                                                                                                                                                                                                                                                                                                                                       primer 304"
                                                                                                                                                                                                                                                                                                               primer 302'
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/note= "ClaI site introd.
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193..201
/*tag= a
209..214
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/note= "ClaI s
172
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                                                                                                                                                                                   (first entry)
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250..242
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119
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                                                                                                                                                                                                      contg. new ClaI sites
                                                                                                                                                                                                                                                                                                                                                                                                                                     Palva IA, Palva AM;
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P-PSDB; AAR21689.
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                                                                                                         241 AGAGGA 246
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AGAGGA 766
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                                                                                                                                                                                   23-JUL-1992
                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                              12-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1990;
                                                                                                                                                                                                                                                   Key
-35<u>signal</u>
                                                                                                                                                                                                                                                                                                                                                                    W09203561-A.
                                                                                                                                                                                                                                                                                     sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                 05-MAR-1992
                                                                                                                                                                                                                                                                       -10_signal
                                                                                                                                                                     AAQ22579;
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AAQ22579
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ATCAGACAGGGTATTTTTTTTTGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGAATAAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCCCGGCACATACGAAAAGACTGGCTGAAAACATTGAGGCCTTTGATGACTGATGATTTGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant genes in a prokaryotic host. The promoter comprises a target module of an enhancer gene operably linked to an initiation module for RNA polymerase. The target module is found in the 5' regulatory region of the apr gene, esp. from B. subtilis. It is a target module of a protein prod. of an enhancer gene esp. the B. subtilis sadd enhancer gene, the sado enhancer gene of B.subtilis, B. amyloliquefaciens or B. licheniformis, or the prtR enhancer gene of B. netto or B. subtilis. The initiation module is that of a gene encoding a prokaryotic excenzyme, esp. B. amyloliquefaciens alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein prodn. using bacillus strain bacteria - by splitting the alpha-amylase bacillus gene, combining the DNA coding for the protein and joining to a plasmid in the bacillus
The inventors claim a new hybrid promoter for the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                     97.5%; Score 242.8; DB 13; Length 537; 99.2%; Pred. No. 4.6e-56; 1ive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                            Sequence 537 BP; 171 A; 90 C; 129 G; 147 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant protein production; secretory peptide; signal sequence; protein secretion; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus amyloliquefaciens alpha-amylase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAN20046 standard; DNA; 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80FI-0004081.
82FI-0000860.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 99.2
Matches 244; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1982-37323E/19.
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(GENE-) GENESIT OY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 AGAGGA 246
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241 AGAGGA 246
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us-09-936-145-1.rng

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121 ATCAGACAGGGTATTTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAATAGGAATAAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Variant alpha amylase enzymes which have improved washing and/or as detergent additives. The enzymes have one or more amino acid residues added, deleted or substituted. The variants can also be used for textile desizing prior to scouring, bleaching and dyeing. The variants have improved thermostability, acid/alkaline stability; low temperature optimum; pH optimum; higher hydrolysis velocity and improved tolerance to other composition constituents, e.g. oxidation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCCCCGCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTGATGACTGATGATTTGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGGGGTTGTTATTTTACTGATATGTAAAATATATATTTGTATAAGAAAATGAGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch; thermostable; methionine; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus; ss.
                                                                                                                                                                                                                                                                                 New Bacillus derived alpha-amylase variants - having amino acion modifications to improve washing and/or dishwashing performance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 242.8; DB 16; Length 2084; Pred. No. 6.4e-56; 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2084 BP; 610 A; 401 C; 544 G; 529 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus amyloliquefaciens alpha amylase gene.
                                                                                                                                                                                         Borchert
                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 72-73; 105pp; English.
                                                                                                                                                                                       Van der zee P, Bisgardfrantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ95032 standard; DNA; 2084
                                       94WO-DK00370
                                                                          93DK-0001133
                                                                                           94DK-0000140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus amyloliquefaciens.
                                                                                                                                                                    Thellersen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 99.2
Matches 244; Conservative
                                                                                                                                 (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                           WPI; 1995-161790/21.
                                                                                                                                                                                                                                              P-PSDB; AAR72448
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AGAGGA 246
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                                       05-OCT-1994;
                                                                                           02-FEB-1994;
                                                                        08-OCT-1993;
20-APR-1995.
                                                                                                                                                                    Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                 ·`
                                           Genomic DNA was isolated from B.amyloliquefaciens and digested with MboI. DNA fragments of 1.5-5.0 x 10power6 daltons were ligated to plasmid pUB110 (isolated from B.subtilis SB202) which had been linearised with BamHI. Recombinant plasmids were used to transform E.subtilis 1A197 (contg. mutuant alpha-amylase gene amy).

Transformants containing the alpha-amylase gene amy).

Transformants containing the alpha-amylase genere were identified and the gene was isolated and sequenced. The secretory signal sequence from the B.mayloliquefaciens alpha-amylase gene was used in the construction of vectors which are useful for the alpha-amylase signal peptide from B.amyloliquefaciens is 10 x more efficient than that from B.amyloliquefaciens is 10 x more efficient than that from B.subtilis. The preferred sequence for use in such vectors covers nucleotides 306 to 349 of AAN20046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGGGTTGTTATTATTACTGATATGTAAAATATATATTGTATAAGAAAATGAGAGGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ATCAGACAGGGTATTTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAATAGGAATAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alpha amylase; variant; enzyme; detergent; additive; dishwashing; washing; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCCCCGCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTGATGACTGATTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                         3; Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus amyloliquefaciens alpha amylase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                  Sequence 576 BP; 190 A; 98 C; 139 G; 149 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                       Score 242.8; DB 3 Pred. No. 4.6e-56;
                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250..1794
/*tag= a
/product= Alpha amylase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ88067 standard; DNA; 2084 BP.
           Claim 9; Page 25; 38pp; French.
                                                                                                                                                                                                                                                                                                                                                                         97.5%;
99.2%;
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343..1791
                                                                                                                                                                                                                                                                                               See also AAN20145-N20154.
                                                                                                                                                                                                                                                                                                                                                                                                           Matches 244; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250..342
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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243 AGAGGA 248
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RESULT 7 AAQ88067 Key

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(first entry)

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AGAGGA 246
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AAX59681;
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NAME OF A COLOR OF A C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 GGGGGGTTGTTATTATTTTACTGATATGTAAATATATTGTATAAGAAAATGAGAGGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of an oxidation stable alpha-amylase - for simultaneous desizing and bleaching or scouring of fabrics contg. starch or starch derivs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCCCCGCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTGATGACTGATTTGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidation stable alpha amylases can be used for the simultaneous desizing and bleaching or scouring of a fabric comprising starch or starch derivatives. They exhibit a better heat stability especially in the presence of oxidising agents. They are obtained from a parent alpha amylase by replacing one or more methionine residues with any amino acid different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or Asp. The parent alpha amylase is derived from a Bacillus species. This sequence encodes the wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity 99.2%; Score 242.8; DB 16; Length 2084; Similarity 99.2%; Pred. No. 6.4e-56; 14; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2084 BP; 610 A; 401 C; 544 G; 529 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Toft AH;
                              250..1794

/*tag= b

/product= Alpha amylase.

250..342

/*tag= c

343..1791
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pedersen HH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 22-24; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type (unmodified) alpha amylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX59681 standard; DNA; 2084 BP
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                                                                                                                                                                                                                                                                                                                                                    94DK-0000141
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1795..2084
/*tag= e
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Marcher D, Nilsson TE,
                    /*tag=
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AGAGGA 246
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                                                                                               sig_peptide
                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                                          10-AUG-1995
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AAX59681
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The specification describes termamyl-like alpha-amylase variants that have altered amino acid sequences to improve properties. The variants are produced by creating one or more of the following mutations in amino acid sequence of the parent termamyl-like alpha-amylase: T141, K142, F143, D144, F145, P146, G147, R148, G149, D174, R181, G182, D168, G169, S170, R171, D168, G169, S170, R171, G172, F173, F267, W268, K269, N270, D271, L272, G273, G273, G274, L275, K311, E346, K385, G456, M457, K458, P459, G460, T461, V462, G463, The variants can be used for washing and/or dishwashing. They can also be used in the production of sweeteners and ethanol from starch, and/or for textile desizing, and in starch liquefaction and/or can function as the parent sequence encodes an amylase that can function as the parent sequence in the production of the variants of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GGGGGGTTGTTATTTTTACTGATATGTAAAATATAAATTTGTATAAGAAAATGAGAGGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCCCCGCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTGATGACTGATTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.5%; Score 242.8; DB 20; Length 2084; 99.2%; Pred. No. 6.4e-56; 2; Indels 0; Mismatches 2; Indels 0;
                                                   Termamyl-like; alpha-amylase; variant; washing; dishwashing; production; sweetener; ethanol; starch; textile desizing; starch liquefaction; saccharification process; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2084 BP; 610 A; 401 C; 544 G; 529 T; 0 other;
DNA encoding a termamyl-like alpha-amylase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borchert TV, Kjaerulff S, Nielsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Termamyl-like alpha-amylase variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 96-97; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                      98WO-DK00471.
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97DK-0001240.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Svendsen A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-326987/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                      30-OCT-1998;
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                                                                                                                                                                            Bacillus sp.
                                                                                                                                                                                                                                                                                             14-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent; dishwashing; laundry; textile; desizing; starch liquefaction; sweetener; ethanol; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 20; Length 2084;
                                                                                                                                                                         Wild type Termamyl(RTM)-like alpha-amylase coding sequence #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - useful as detergents or for textile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2084 BP; 610 A; 401 C; 544 G; 529 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.5%; Score 242.8; DB 20
99.2%; Pred. No. 6.4e-56;
iive 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Svendsen A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 81-82; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borchert TV,
                         AAX57596 standard; DNA; 2084 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                desizing or starch liquefaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-DK00444.
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                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Variant alpha-amylases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-277632/23.
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                                                                                                                        16-JUL-1999
                                                                                                                                                                                                                                                                                                                      Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-1999
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AAX57596
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The present sequence encodes a parent alpha-amylase from which mutants with increased stability at acidic pH, low calcium concentration and high temperatures have been derived. The sequence was isolated from a Bacillus amyloliquefaciens genomic DNA library. A variant may contain mutations in one or more solvent exposed amino acid residues to increase the overall hydrophobicity of the enzyme or the overall number of methyl groups in the side chains of exposed residues may be increased. The mutations can be incorporated by site-directed mutagenesis or by random mutagenesis. As a result of their increased stability, the variants are suitable for the industrial processing of starch, i.e. starch liquefaction and textile desizing. Hybrid alpha-amylases comprising partial amino acid sequences derived from two or more alpha-amylases have also been created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Variant of parent termamyl-like alpha amylase useful for washing, textile desizing and starch liquefaction, comprising alterations in one or more solvent exposed amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ATCAGACAGGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAATAGGAATAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                         sednence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 242.8; DB 21; Length 2084;
Pred. No. 6.4e-56;
); Mismatches 2; Indels 0;
                                                                                                                        Bacillus amyloliquefaciens Termamyl-like alpha-amylase DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bisgard-Frantzen H, Andersen
                                                                                                                                                                                                                                                                                              "Termamyl-like alpha-amylase"
                                                                                                                                                   Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction; saccharification; mutein; mutant; enzyme stability; hybrid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2084 BP; 610 A; 401 C; 544 G; 529 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 75-76; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in order to increase enzyme stability
                                                                                                                                                                                                                                                Location/Qualifiers
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                             AAA48484 standard; DNA; 2084
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                                                                                                                                                                                                                   Bacillus amyloliquefaciens
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/product= '
                                                                                         (first entry)
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                                                                                                                                                                                                                                                                343..1794
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Matches 244; Conservative
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                                                                                                                                                                                                                                                                                                                                             WO200029560-A1.
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                                                                                         04-SEP-2000
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                                                          AAA484;
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Best Local 9
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RESULT 11
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                          GCCCCGCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTGATGATGATTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to variants of a parent Termamyl-like alpha-amylases. These are used for starch liquefaction, ethanol production, detergent, and textile desizing. The amylases have altered stability, particularly at high temperatures from 70\text{-}120\text{plusoC} and low pH in the range from pH 4.0\text{-}6.0. The present sequence is a termamyl-like-alpha-amylase encoding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               production, washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful in detergent
GGGGGGTTGTTATTTTACTGATATGTAAAATATATATTTGTATAAGAAATGAGGGG
                                                                                                                                                                                                                                                                        .; alpha amylase; starch liquefaction; ethanol production; desizing; detergent; enzyme; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.5%; Score 242.8; DB 24; Length 2084; 99.2%; Pred. No. 6.4e-56; Live 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "termamyl-like alpha amylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2084 BP; 610 A; 401 C; 544 G; 529 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fuglsang CC;
                                                                                                                                                                                                                                                  Termamyl-like-alpha-amylases encoding sequence #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               compositions, for starch liquefaction, ethanol and/or dish washing, and textile desizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variant of parent Termamyl-like alpha amylase,
                                                                                                                                                                                                                                                                                                                                                                                       /partial
/note= "no start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Andersen C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 69-71; 90pp; English.
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                          ABL96211 standard; DNA; 2084 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-2000; 2000DK-0001354.
10-NOV-2000; 2000DK-0001687.
26-APR-2001; 2001DK-0000655.
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                                                                                                                                                                                                                                                                                                             Bacillus amyloliquefaciens.
                                                                                                                                                                                                                           (first entry)
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Matches 244; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T, Kjaerulff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOVO ) NOVOZYMES AS
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241 AGAGGA 246
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                                                                                                                                                                                                                                                                            Termamyl;
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The present invention describes a variant of a parent termamyl-like abhar-amylase (EC 3.2.1.1) (I) comprising an alteration at one or more positions of a group of 31 possible amino acid positions. The alteration in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184, Gly186, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306, Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444, Asn445, Lys446, Gln449, Arg458, Asn471, or Asn484. (I) can be used for
                                                                                                                                                                                                                                                                       Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1; variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent; washing; sweetener; ethanol; starch; gene; ds.
                                                                                                                                                                                                                                            B. amyloliquefaciens termamyl-like alpha-amylase encoding DNA SEQ ID:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel variant of parent termamyl-like alpha-amylase useful as a component in washing and dishwashing compositions, for textile desizing, for starch liquefaction, and for producing sweeteners and
/EC_number= "3.2.1.1"
/product= "Termamyl-like alpha-amylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 143-145; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TV, Nielsen BR;
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
343..1794
/*tag= a
                                                                                                                                                    ABL50568 standard; DNA; 2084 BP
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2000US-189857P.
2001DK-0000303.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2001; 2001US-271382P
                                                                                                                                                                                                                                                                                                                                    Bacillus amyloliquefaciens
                                                                                                                                                                                                              (first entry)
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P-PSDB; ABB06937.
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                                            AGAGGA 246
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washing and/or dishwashing, textile desizing, and starch liquefaction. (I) is useful as a component in hard surface cleaning detergent composition, and for producing sweetners and ethanol from starch. (I) has altered solubility, preferably increased solubility, in particular under washing, dish washing or hard surface cleaning conditions. The present sequence encodes a Bacillus amyloliquefaciens termamyl-like alpha-amylase which is used in the exemplification of
                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                       ATCAGACAGGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGAATAAA 180
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                                                                                                                                  1 GCCCCGCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTGATGACTGATTTGG 60
                                                                                                                                                                                                                                                                                                                                                                                                           Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup; starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink; bakery; cereal bar; ice cream; coffee whitener; salad dressing; cured meat; fermented meat; spice; ss.
                                                                                                                                          GGGGGGTTGTTATTTTACTGATATGTAAAATATAATTTGTATAAGAAAATGAGAGGG
                                                                                               Score 242.8; DB 24; Length 2084;
Pred. No. 6.4e-56;
0; Mismatches 2; Indels 0;
                                                                              Sequence 2084 BP; 610 A; 401 C; 544 G; 529 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Alpha-amylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       AAI72215 standard; cDNA; 2084 BP
                                                                                                                                                                                                                                                                                                                                                                                            Bacillus alpha amylase BAN cDNA.
                                                                                                97.5%;
99.2%;
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2000US-212852P.
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                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus amyloliquefaciens
                                                                                             Query Match
Best Local Similarity 99.2
Matches 244; Conservative
                                                             the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nielsen BR, Weibye M;
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P-PSDB; AAB47854.
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20-JUN-2000;
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The sequences given in AAI72211-16 encode modified alpha-amylases derived from the genus Bacillus. These alpha amylases are Termamyl-
is alpha-amylase and they have been pre-oxidized. The alpha amylase is useful for producing a maltodextrin or glucose syrup, by treating starch with a pre-oxidized alpha-amylase until a product with a nelecular weight of between 5-30 kda has been provided. The product comprises a maltodextrin with a DE of 18.5 and/or a maltodextrin with a nelecular weight of the for a maltodextrin with a DE of 18.5 and/or a maltodextrin with a nelecular weight of 14-16 kda. The alpha amylase is useful for producing maltodextrin or glucose syrup, where the glucose syrup is useful as an ingredient in food, feed or pharmaceuticals. Glucose syrup is useful in confectionery such as candies, beverages such as isotonic drinks, whiteners, conventional foods such as salad dressings, and food and confidents and preparations such as cured meat, fermented meat, spices
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
New modified alpha-amylase derived from the genus Bacillus and/or is a Termamyl-like alpha-amylase, which has been pre-oxidized for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TERMAMYL; alpha-amylase; ds; detergent; dishwashing; textile desizing; starch liquefaction; ethanol production; hard surface cleaner; sweetener; amylopectin; limit dextrin; NOVAMYL; BAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCAGACAGGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGAATAAA 180
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Pred. No. 6.4e-56;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2084 BP; 610 A; 401 C; 544 G; 529 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus DNA encoding TERMAMYL-like alpha-amylase BAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Alpha-amylase BAN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and seasoning encapsulated flavours.
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                                                                                                          Claim 7; Page 37-39; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                     maltodextrin or glucose syrup
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99.28;
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Best Local Similarity 99.2
Matches 244; Conservative
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The invention relates to a variant of parent TERMANYL-like alpha-
amylase comprising an alteration at regions 186-193, 261-276, 283-293 or
334-339, or at position 224, where the variant has alpha-amylase activity
and each position corresponds to a position of a parent Termanyl-like
alpha-amylase sequence having a Bacillus licheniformis alpha-amylase
sequence of 483 amino acids, given in specification. The variant alpha-
amylase, a detergent additive comprising the variant or a detergent
composition comprising the variant, is useful for washing and/or
dishwashing or textile desizing. The alpha-amylase is useful for starch
cliquefaction or ethanol production and as a component in a hard surface
cleaning detergent composition, and for producing sweeteners from starch.
The variant has altered alpha-1, 6D-glucosidic branch linkage
cleavage activity on amylopectin, preferably increased alpha-1,
6D-glucosidic branch linkage cleavage activity of amylopectin or a
limit dextrin prepared by TERMANYL (RTM) or NOVAMYL (RTM). The
                                                                                                                                                                                                                                                                                                                                    New variant of parent Termamyl-like alpha-amylase for use as a component in washing and dishwashing compositions, for textile desizing, for starch liquefaction, and for producing sweeteners and ethanols from starch
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                                                                                                                                                                                                                                 Nielsen BR;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 68-72; 84pp; English.
                                                                                                    10-MAY-2001; 2001WO-DK00323.
                                                                                                                                            12-MAY-2000; 2000DK-0000779
                                                                                                                                                                                                                               Svendsen A, Jorgensen CT,
                                                                                                                                                                                        (NOVO ) NOVOZYMES AS
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P-PSDB; AAU12153.
                   WO200188107-A2
                                                           22-NOV-2001.
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121 ATCAGACAGGGTATTTTTATGCTGTCCCAGACTGTCCGCTGTGTAAAAAATAGGAATAAA 180
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                                                   1 GCCCCGCACATACGAAAGACTGGCTGAAAACATTGAGCCTTTGATGATGATGATTTGG 60
 Best Local Similarity 99.2
Matches 244; Conservative
Similarity
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AGAGGA 246

δ

AGAGGA 246 241

Search completed: February 21, 2003, 07:20:48 Job time: 231 secs

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VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
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FEATURES
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AR168304
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No. is the number of results predicted by chance to have a Pred.

M. Unclassified.
Unclassified.
El (bases 1 to 2604)

S Norman, B.Edmund. and Hendriksen, H. Vang.
Enzymatic preparation of glucose syrup from starch
Enzymatic preparation of 311-SEP-2001;
Location/Qualifiers

PAT 17-DEC-2001

linear

DNA

AR168304 2604 bp Sequence 3 from patent US 6287826.

AR168304

AR168304 AR168304.1 GI:17904148

Jnknown.

ALIGNMENTS

M36664 Synthetic p M3665 Synthetic p M34931 Synthetic B A01100 Nucleotide A0491 Artifictal M35837 C.tetragono Y13644 Chlorogoniu AR168304 Sequence AX036892 Sequence V00092 Bacillus am A00155 Nucleotide A00156 Nucleotide A00604 B.amylolique A00605 B.amylolique A00605 B.amylolique A00605 B.amylolique A00605 B.amylolique A00605145 Sequence AR037275 Sequence AR129916 Sequence AR13905 Sequence AX390502 Sequence AX390502 Sequence AX390502 Sequence AX39050 Sequence AX30501 Sequence AX30501 Sequence AX08819 Sequence AX08819 Sequence 24 140895 Sequence 24 15687 Sequence 24 140895 Sequence 24 140895 Sequence AX088921 Sequence AX088921 Sequence AX088920 Sequence AX088920 Sequence AX080920 Sequenc AC023934 Homo sapi AC021010 Homo sapi AC062006 Homo sapi score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES E00040 AX167074 SYNPTUB261 SYNPTUB263 SYNBACAMY A01100 A04541 SYNAAAGEP AR129916 AR137905 AR143262 AX244195 AX305020 AX3339268 AX370717 A00157 A00158 A00158 AR160501 AX088919 140596 140867 140895 156837 AX160503 AX088921 AX088920 AX088920 AC023934 AC021010 AC062006 DB 20084 20084 20084 20084 5776 1185 1162 157069 187599 181062 162 185 185 185 185 465 465 13222 Length 2084 2084 2084 Query Match Score 158.8 158.8 158.8 157.2 157.2 157.2 155.6 51.2 46.4 46.4 46.4 Result õ

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Bacillus amyloliquefaciens
Bacillus amyloliquefaciens
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
1 (bases 1 to 2604)
Svendsen,A., Andersen,C., Bisgaard-Frantzen,H., Joergensen,C.T. and
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YANELSLDGFRIDDAKHIKFSFLRDWYQARRQATGKEMFTYABYWDNNAGKLENYLNK
TSFNGSVFDVPLHFNLQAASSGGGGYDMRRLLDGTVVSRHPERAVTFVENHDTQPGGS
LESTWQTWRFRLAYFILTRESGYPOVFYGDNYGTKGTSPREIPSLKDNIEPILKARK
EYAYGPQHDYIDHPDVIGWTREGDSSAAKSGLAALITDGFGGSKRMYAGLKNAGETWY
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HKAGADATEDYTAVEVNPANRNOETSEEYOIKAWTDFRFPGRGNTYSDFKWHWYHFDG
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/db_xref="taxon:1390"
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                                                            98.8%; Score 246; DB 6; 100.0%; Pred. No. 6.2e-49; ive 0; Mismatches 0;
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/note="unnamed protein product"</pre>
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Patent: WO 0060059-A 5 12-0cT-2000;
NOVONORDISK AS (DK)
Location/Qualifiers
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/db_xref="GI:11226327"
         /organism="unknown"
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amylase: amylase-lpha; signal peptide.
Bacillus amyloliquefaciens.
Bacillus amyloliquefaciens.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
1 (bases 1 to 537)
Palva, I., Pettersson, R.F., Kalkkinen, N., Lehtovaara, P., Sarvas, M., Soderlund, H., Takkinen, K. and Kaariainen, L.
Nucleotide sequence of the promoter and NH2-terminal signal peptide region of the alpha-amylase gene from Bacillus amyloliquefaciens
B2051296
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/transl_table=11
/transl_table=11
/protein_id="Cal-139298"
/db_xref="G1:39298"
/db_xref="G1
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Bacillus amyloliquefaciens gene fragment encoding alpha-amylase.
(EC 3.2.1.1).
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/organism="Bacillus amyloliquefaciens"
/db_xref="taxon:1390"
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                               Score 246; DB 6;
Pred. No. 6.2e-49;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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                                                                                                                                                                   576 bp DNA linear
m patent number GB2133408
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                                                                                                                                                                                                                                                       Palva,I.
Patent: GB 2133408-A 1 25-JUL-1984;
Ikka Palva
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/organism="Bacillus
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PAT 16-FEB-1993
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Bacillus amyloliquefaciens
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/organism="Bacillus amyloliquefaciens"
/db_xref="taxon:1390" 149 t
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99.2%; Pred. No. 4.6e-48;
live 0; Mismatches 2;
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Pred. No. 4.6e-48;
0; Mismatches 2;
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Patent: GB 2133408-A 2 25-JUL-1984;
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                                             1. 576 /
/organism="Bacillus sp."
/db_xref="taxon:1409"
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Bacillus amyloliquefaciens alpha-amylase gene, complete cds.

JO1542.1 GI:142428

Bacillus amyloliquefaciens Marburg strain-ih, cDNA to mRNA.

Bacillus amyloliquefaciens

Bacillus amyloliquefaciens

Bacillus amyloliquefaciens

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Soderlund, H., Takkinen, K. and Kaariainen, L. httovaara, P., Sarvas, M., Soderlund, H., Takkinen, K. and Kaariainen, L. etchtovaara, P., Sarvas, M., Soderlund, H. acquence of the promoter and NH2-terminal signal peptide region of the alpha-amylase gene from Bacillus amyloliquefaciens
                                                                        PAT 13-APR-1993
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                                                    S76 bp DNA linear PAT 13-
B.amyloliquefaciens alpha-amylase gene, reverse complement.
A00605.
A00605.1 GI:14541
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Bacillus amyloliquefaciens
Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus
Location/Qualifiers
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Takkinen, K., Pettersson, R.F., Kalkkinen, N., Palva, I.,
and Kaariainen, L.
                                                                                                                                                                                                                                                                                                   Length
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/db_xref="taxon:1390"
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Pred. No. 4.6e-48;
0; Mismatches 2;
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sal Similarity 99.2%;
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/transl_table=11
/protein_id="AAA22191.1"
/protein_id="AAA229.1"
/db_xref="GI:142429"
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PNDGQHWKRLQNDAEHLSDIGITAWWIPPAYKGLSGSDNGYGFYDLYDLGEFQQKGTV
RTKYGTKSELQDQAIGSLHSRNQYKGDWVANNHARAGADATEDVTAVEVNPANRNQETSE
EYQIKAWTDERFPGRGWTYSDFKWHWYHFDGADWDESRKISRIFRFRGEGKAWDWEVS
SENGNYDXLMYADDVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSFLRDWV
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MRKLLDGYVXSRHPEKAVTFVENHDYQPGQSLESTYQTWFFNATAYFLITRESGYPQV
FYGDWYGTKGTSPKTETSLKDN IEPTLIKAREYAYGPQHDYTDHPDVIGWTREDSSA
AKSGLAALITDGPGGSKRMYAGLKNAGETWYDLTGNRSDTVKIGSDGWGEFHVDDSSA
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                                                                                                                                                                       The deduced amino acid sequence deviates slightly from a published sequence for this species (four conflicts). the signal peptide seems unusually large (31 residues) compared to other known signal peptides. the promoter and mRNA start point are speculatively addressed.
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Lehtovaara,P., Ulmanen,I. and Palva,I. In vivo transcription initiation and termination sites of alpha-amylase gene from Bacillus amyloliquefaciens cloned Bacillus subtilis Gene 30 (1-3), 11-16 (1984)
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343. .1791
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Pred. No. 3.7e-48;
0; Mismatches 2;
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250. 1794
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AR008285
AR008285.1 GI:3967394
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Best Local Similarity 99.2%;
Matches 244; Conservative
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REFERENCE AUTHORS JOURNAL

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BASE COUNT ORIGIN

PAT 29-SEP-1999

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Svendsen, A., Bisg.ang.rd-Frantzen, H. and Borchert, T. Vedel. alpha.amylase mutants
Patent: 15 599169-A 3 23-NOV-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                      1 (bases 1 to 2084)
Bisg.ang.rd-Frantzen, H., Borchert, T. Vedel., Svendsen, A., Thellersen, M. and Van der Zee, P.
Amylase variants
Patent: US 5830837-A 3 03-NOV-1998;
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Pred. No. 3.7e-48;
0; Mismatches 2;
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Sequence 3 from patent US 5830837.
AR052145.1 GI:5975509
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Sequence 3 from patent US 5989169.
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1. .2084
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1 401 c 544 g
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AR087551.1 GI:10014314
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99.28;
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Matches 244; Conservative
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                                1 (bases 1 to 2084)
Bisgard-Frantzen, H., Borchert, T. Vedel., Svendsen, A., Thellersen, M. and Van der Zee, P.
Amylase variants
Patent: US 5753460-A 3 19-MAY-1998;
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Bisg.ang.rd-Frantzen,H., Borchert,T.Vedel., Svendsen,A.,
Thellersen,M. and Van der Zee,P.
Amylase variants
Patent: US 5801043-A 3 01-SEP-1998;
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AR137905
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Svendsen A., Borchert.T.Vedel. and Bisg.ang.rd-Frantzen,H.
anpha.amylase mutants
Patent: US 6187576-A 13 13-FEB-2001;
Location/Qualifiers
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                                       Score 242.8; DB 6;
Pred. No. 3.7e-48;
0; Mismatches 2;
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Pred. No. 3.7e-48;
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                                        Query Match 97.5%;
Best Local Similarity 99.2%;
Matches 244; Conservative
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Matches 244; Conservative
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          PAT 16-JUN-2001
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                                                                                                                                     1 (bases 1 to 2084)
Svendsen,A., Kjaerulff.S., Bisgaard-Frantzen,H. and Andersen,C.
alpha.-Amylase variants
Patent: US 617565-A 31 06-MAR-2001;
Location/Qualifiers
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Borchert T.Vedel., Svendsen, A., Andersen, C., Nielsen, B., Nissen, T.Lauesgaard. and Kj.ae butted.rulff, Sslashedren. alpha.-amlase mutants
Patent: US 6204232-A 58 20-MAR-2001;
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Pred. No. 3.7e-48;
0; Mismatches 2;
Sequence 31 from patent US 6197565. AR137905 GI:14479414
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Best Local Similarity 99.2%;
Matches 244; Conservative (
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Matches 244; Conservative
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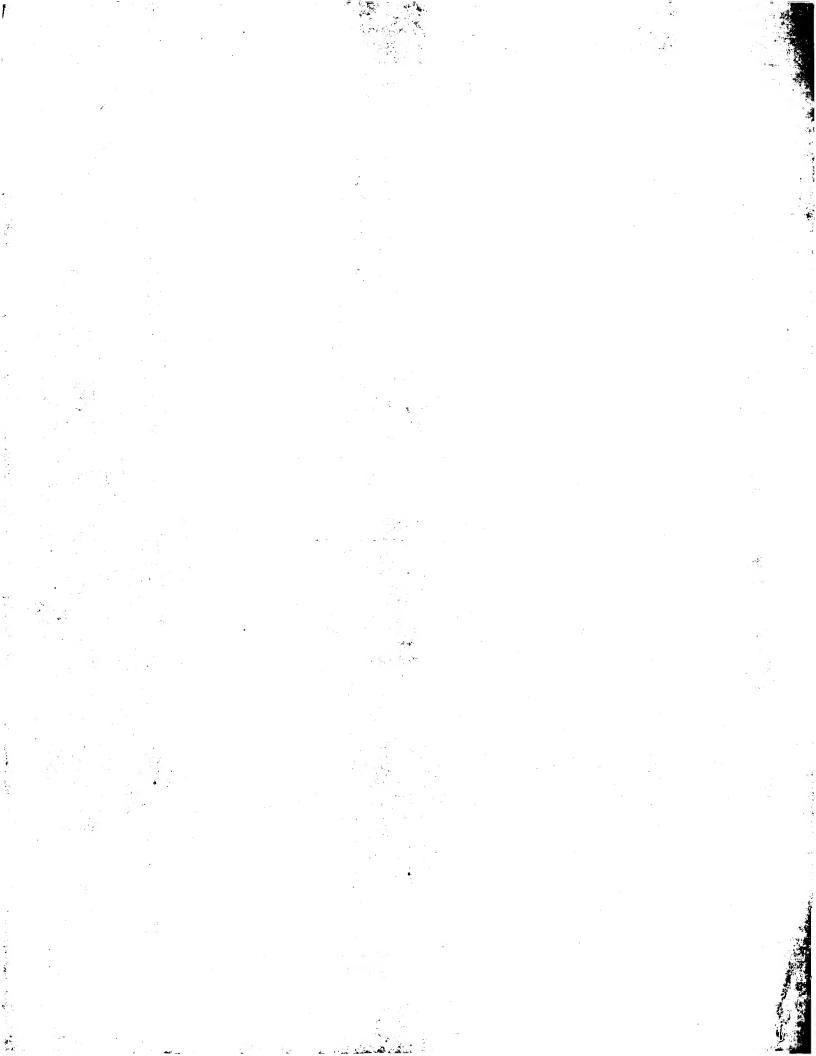
0y	61 CTGAAGAAGTGGATGGATTGTTTGAGAAAGAAGAAGAAGCATAAAAAATACCTTGTCTGTC
qc	61 CTGAAGAAGTGGATCGATTGTTTGAGAAAAAGAAGAACCATAAAAATACCTTGTCTGTC
0y 1	121 ATCAGACAGGGTATTTTTATGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGAATAAA 180

οp

Qy Db

²⁴¹ AGAGGA 246 ||||||| 241 AGAGGA 246 Qy Db

Search completed: February 21, 2003, 07:40:17 Job time : 1159 secs



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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
```

```
(without alignments)
2660.637 Million cell updates/sec
                                        February 21, 2003, 07:16:56; Search time 2353 Seconds
nucleic search, using sw model
OM nucleic
                                        Run on:
```

sed:

sed:

2_6/ptodata/1/pna/US6001_COMB.sc 2_6/ptodata/1/pna/US6002_COMB.sc 2_6/ptodata/1/pna/US6003_COMB.sc 2_6/ptodata/1/pna/US6004_COMB.sc 2_6/ptodata/1/pna/US6005_COMB.sc 2_6/ptodata/1/pna/US6006_COMB.sc 2_6/ptodata/1/pna/US6007_COMB.sc

sed: sed:

sed:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 US-09-936-145-1 249 Scoring table: Perfect score: Sequence:

24791104 seqs, 12571243825 residues Searched:

of hits satisfying chosen parameters: seq length: 0 seq length: 200000000 Total number Minimum DB Maximum DB

49582208

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pending_Patents_NA_Main:*

1: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/USO7_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/USO7_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/USO8_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/USO81_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/USO81_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/USO83_COMB.seq:*
8: /cgn2_6/ptodata/1/pna/USO83_COMB.seq:*
9: /cgn2_6/ptodata/1/pna/USO83_COMB.seq:*
10: /cgn2_6/ptodata/1/pna/USO83_COMB.seq:*
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17: /cgn2_6/ptodata/1/pna/USO83_COMB.seq:*
18: /cgn2_6/ptodata/1/pna/USO83_COMB.seq:* Database

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sed:
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/cgn2_6/ptodata/1/pna/US6037_COMB.seq:
/cgn2_6/ptodata/1/pna/US6037_COMB.seq:
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/cgn2_6/ptodata/1/pna/US6031_COMB.seq
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/cgn2_6/ptodata/1/pna/US6033_COMB.seq
/cgn2_6/ptodata/1/pna/US6033_COMB.seq
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CGGG 2.6 (Ptodata/I/pna/US6003_COMB. Sec
CGGG 2.6 (Ptodata/I/pna/US6003_COMB. Sec
CGGG 2.6 (Ptodata/I/pna/US6004_COMB. Sec
CGGG 2.6 (Ptodata/I/pna/US6005_COMB. Sec
CGGG 2.6 (Ptodata/I/pna/US6007_COMB. Sec
CGGG 2.6 (Ptodata/I/pna/US6010_COMB. Sec
CGGG 2.6 (Ptodata/I/pna/US6010_COMB. Sec
CGGG 2.6 (Ptodata/I/pna/US6011_COMB. Sec
CGGG 2.6 (Ptodata/I/pna/US6012_COMB. Sec
CGGG 2.6 (Ptodata/I/pna/US6021_COMB. Sec
CGGG 2.6 (Ptodata/I/pna/US6022_COMB. Sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/pna/US6033_COMB.
/cgn2_6/ptodata/1/pna/US6034_COMB.
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/cgn2_6/ptodata/1/pna/US6036_COMB.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/1/pna/US091_COMB.seq:*/cgn2_6/ptodata/1/pna/US092_COMB.seq:*/cgn2_6/ptodata/1/pna/US093_COMB.seq:*/cgn2_6/ptodata/1/pna/US094_COMB.seq:*/cgn2_6/ptodata/1/pna/US094_COMB.seq:*/cgn2_6/ptodata/1/pna/US095A_COMB.seq:*/cgn2_6/ptodata/1/pna/US095B_COMB.seq:*/

18: 19: 20: 21:

/cgn2_6/ptodata/1/pna/US089_COMB.seq:* /cgn2_6/ptodata/1/pna/US090_COMB.seq:*

/cgn2_6/ptodata/1/pna/US095C_COMB.seq /cgn2_6/ptodata/1/pna/US095C_COMB.seq /cgn2_6/ptodata/1/pna/US096A_COMB.seq /cgn2_6/ptodata/1/pna/US096B_COMB.seq /cgn2_6/ptodata/1/pna/US096B_COMB.seq /cgn2_6/ptodata/1/pna/US096B_COMB.seq /cgn2_6/ptodata/1/pna/US096B_COMB.seq

223: 224: 226: 227: 228: 30:

/cgn2_6/ptodata/1/pna/US097A_COMB.seq. /cgn2_6/ptodata/1/pna/US097B_COMB.seq. /cgn2_6/ptodata/1/pna/US097C_COMB.seq. /cgn2_6/ptodata/1/pna/US098A_COMB.seq. /cgn2_6/ptodata/1/pna/US098B_COMB.seq.

/cgn2_6/ptodata/1/pna/US099B_COMB.seq: /cgn2_6/ptodata/1/pna/US099C_COMB.seq: /cgn2_6/ptodata/1/pna/US099D_COMB.seq:

331... 334... 336... 336... 40...

ptodata/1/pna/US100A_COMB.

/cgn2_6 /cgn2_6

/cgn2_6/ptodata/1/pna/US102A_COMB.seq: /cgn2_6/ptodata/1/pna/US102B_COMB.seq:

/cgn2_6/ptodata/1/pna/US098C_COMB.seq: /cgn2_6/ptodata/1/pna/US099A_COMB.seq:

Description	Sequence 1, Appli		Sequence 5, Appli	Sequence 3, Appli	3,	ω,	3, 7	m	'n	Sequence 3, Appli	31,	Seguence 31, Appl	Sequence 13, Appl	3, A	Sequence 3, Appli	Sequence 58, Appl	Sequence 9, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 3, Appli	Sequence 3, Appli
ID	US-09-936-145-1	US-09-936-145-2	US-10-146-327-5	US-08-458-387-3	US-08-600-908-3	US-08-683-838-3	US-09-096-087-3	US-09-325-603-3	US-09-327-563-3	US-09-327-563B-3	US-09-441-313-31	US-09-441-313A-31	US-09-545-586-13	US-09-648-826-3	US-09-648-826A-3	US-09-769-864-58	US-09-854-346-9	US-09-918-543-9	US-09-925-576C-9	US-10-184-771-3	US-10-186-042-3
DB	35	35	40	æ	10	10	14	17	17	17	18	18	21	25	25	30	32	34	34	41	41
Query Match Length DB	249	270	2604	2084	2084	2084	2084	2084	2084	2084	2084	2084	2084	2084	2084	2084	2084	2084	2084	2084	2084
Query	100.0	100.0	98.8	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5
Score	249	249	246	242.8	242.8	242.8	242.8	242.8	242.8	242.8	242.8	242.8	242.8	242.8	242.8	242.8	242.8	242.8	242.8	242.8	242.8
Result No.	1	7	e	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21

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                                                   Sequence 49, Appl
Sequence 59, Appl
Sequence 1927, Appl
Sequence 227, Appl
Sequence 277, Appl
Sequence 1737, Appl
Sequence 1737, Appl
Sequence 349, Appl
Sequence 349, Appl
Sequence 349, Appl
Sequence 385, Appl
Sequence 58207, Appl
Sequence 353, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ATCAGACAGGGTATTTTTAFGCTGTCCAGACTGTCCGCTGTGTAAAAAATAGGAATAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
100.0%; Score 249; DB 35;
100.0%; Pred. No. 1.5e-53;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FUSHINI, Nacya
APPLICANT: FUSHINI, Nacya
APPLICANT: Mizubuchi, Hiroyuki
APPLICANT: Obshina, Yoshie
APPLICANT: Obshina, Yoshie
APPLICANT: Tamamoco, Yoshie
APPLICANT: Asstrake, Nozomu
APPLICANT: Miyoshi, Shinsuke
TITLE OF INVENTION: Promoters
FILE REFERENCE: 3274-011309
CURRENT APPLICATION NUMBER: US/09/936,145
CURRENT FILING DATE: 2001-09-07
PRIOR PILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Word 97 SR-2
SEG ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5-09-936-145-1
Sequence 1, Application US/09936145
GENERAL INFORMATION:
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Best Local 3
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240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GCCCCGCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTGATGACTGATTTGG 60
 GGGGGGTTGTTATTATTTACTGATATGTAAAATATATTTGTATAAGAAAATGAGGGG
                     GGGGGGTTGTTATTATTACTGATATGTAAAATATAATTTGTATAAGAAAATGAGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 249; DB 35;
100.0%; Pred. No. 1.6e-53;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                     APPLICANT: Incoue, Yasushi
APPLICANT: Fushini, Naoya
APPLICANT: Fushini, Naoya
APPLICANT: Mizubuchi, Hiroyuki
APPLICANT: Yamamoto, Yoshie
APPLICANT: Yamamoto, Yoshie
APPLICANT: Obshima, Yoshie
APPLICANT: Yasutake, Nozomu
APPLICANT: Yasutake, Nozomu
APPLICANT: Myoshi, Shinsuke
TITLE OF INVENTION: Promoters
FILE REFERENCE: 3274-011309
CURRENT APPLICATION NUMBER: US/09/936,145
PRIOR APPLICATION NUMBER: US11/060904
PRIOR PILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 22
SEQ ID NOS: 22
SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/10146327
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Jorgensen, Christel T.
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Kjaerulff, Soren
                                                                                                                                                                                                          Sequence 2, Application US/09936145 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 249; Conservative
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US-09-936-145-2
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ATTORNEY/AGENT INFORMATION:
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| AGAGGA 246
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FEATURE:
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LOCATION:
US-08-458-387-3
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COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                        98.8%; Score 246; DB 40;
100.0%; Pred. No. 1.8e-52;
ive 0; Mismatches 0;
                                             CURREMY FILING DATE: 2002-05-15.
PRIOR APPLICATION NUMBER: US/09/537,168
PRIOR PILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FeatSEQ for Windows Version 4.0
SSET DENOS FILING DATE: 1999-04-01
TITLE OF INVENTION: Alpha-Amylase Variants FILE REFERENCE: 5886.200-US CURRENT APPLICATION NUMBER: US/10/146,327
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APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pla
TITLE OF INVENTION: AMYLASE VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/343,804 FILING DATE: 22-NOV-1994
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FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                       ; TYPE: DNA; ORGANISM: Bacillus amyloliquefaciens US-10-146-327-5
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Best Local Similarity 100.
Matches 246; Conservative
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PRIOR APPLICATION DATA:
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New York
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US-08-458-387-3
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STATE:
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Pred. No. 1.1e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Novo Nordisk of North America, Inc. 405 Lexington Avenue, 64th Floor
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                                       4054.214-US
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APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Brochert, Torben Vedel
TITLE OF INVENTION: 'Amylase Mutants
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York COUNTRY: United States of America ZIP: 10174-6401 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
NAME: Lowney Dr., Karen A.
REGISTRATION UNDRER: 31,274
REFERENCE/DOCKET UNDRER: 4054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2084 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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; GENERAL INFORMATION:
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99.2%;
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ADDRESSEE: Novo Nord
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Best Local Similarity
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STREET: 400...
TTTY: New York
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RESULT 7
US-09-096-087-3
Sequence 3, Application US/09096087
Sequence 3, Application US/09096087
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendench, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
FILING DATE: 18-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.5%;
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ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 99.2%
Matches 244; Conservative
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343..1791
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250..342
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AGAGGA 246
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LOCATION:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.5%; Score 242.8; DB 10; Length 2084; 99.2%; Pred. No. 1.1e-51; Live 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of America
LIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Novo Nordisk of North America, Inc. STREET: 405 Lexington Avenue, 64th Floor CITY: New York
                ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4394.204-US
TELEPHONICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPKX: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2084 base pairs
TYPE: nucleic acid
STRANEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-08-683-838-3
Sequence 3, Application US/08683838
SEQUENCE 1. APPLICANTION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
TITLE OF INVENTION: '-Amylase Mutants;
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 99.2
Matches 244; Conservative
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250..342
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STATE: New York
      CLASSIFICATION:
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LOCATION:
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; LOCATION:
US-08-600-908-3
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·181 GGGGGGTTGTTATTTTACTGATATGTAAAATATATATTTGTATAAGAAAATGAGAGGG 240
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Pred. No. 1.1e-51;
0; Mismatches 2;
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ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUBER: 33,728
REFERENCE/DOCKET NUMBER: 4394.400-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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United States of America
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NUMBER OF SEQUENCES:
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241 AGAGGA 246
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   COUNTRY:
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99.2%; Pred. No. 1.1e-51;
Live 0; Mismatches 2; Indels
              SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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APPLICANT: Bigg rd-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
                                                                                      PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: LOWNEY DF., KATEN A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-US
TELEPONMUNICATION INFORMATION:
TELEPHONE: 12-867-0123
TELEFAS: 212-867-0123
TELEFAS: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2084 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                             us/09/096,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09325603 GENERAL INFORMATION:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 99.2
Matches 244; Conservative
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250..342
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343..1791
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250..1794
                                                           APPLICATION NUMBER: FILING DATE:
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241 AGAGGA 246
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LOCATION:
FEATURE:
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LOCATION:
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US-09-096-087-3
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CITY: Ne
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                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/325,603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: -Amylase Mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/600,908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0555
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COUNTAL ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CAMPHITER: IBM PC COMPALIBLE
CAMPHITER: ACTUALIBLE
CAMPHITER: ACTUAL COMPALIBLE
CAMPHITER: ACTUAL COMPACTION COMPA
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MOLECULE TYPE: DNA (genomic)
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250..1791
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1 GCCCCGCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTGATGACTGATTTGG
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             APPLICANT: Bisgard Frantzen, Henrik APPLICANT: Bisgard Frantzen, Henrik APPLICANT: Borchert, Torben Vedel TITLE OF INVENTION: Alpha-Amylase Mutants; FILE REFERENCE: 0776/1F216-US2 CURRENT APPLICATION NUMBER: US/09/327,563B; CURRENT FILING DATE: 1999-06-08 PRIOR FILING DATE: 1996-07-18 NUMBER OF SEQ ID NOS: 16 SOFTWARE: FastSEQ for Windows Version 3.0 SED ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Andersen, Carsten
TITLE OF INVENTION: -Amylase Variants
FILE REFRENCE: 5709,000-02
CURRENT APPLICATION NUMBER: US/09/441,313
CURRENT FILING DATE: 1999-11-16
EARLIER APPLICATION NUMBER: 09/193,068
EARLIER FILING DATE: 1998-11-16
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 3.0
SSOFTWARE: FASTSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                  ORGANISM: B. amyloliquefaciens;
FEATURE:
NAME/KEY: CDS
LOCATION: (250)...(1791)
NAME/KEY: mat_peptide
LOCATION: (343)...(1791)
NAME/KEY: sig_peptide
LOCATION: (250)...(342)
US-09-327-563B-3
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; ORGANISM: B. amyloliquefaciens
US-09-441-313-31
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| AGAGGA 246
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US-09-441-313-31
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COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/327,563
FILING DATE:
               E: Novo Nordisk of North America, Inc. 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/600,908
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRON: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHRRACTERISTICS: LENGTH: 2084 base pairs TYPE: nucleic acid STRANDEDNESS: single
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MOLECULE TYPE: DNA (genomic)
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CORRESPONDENCE ADDRESS
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AGAGGA 246
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LOCATION:
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NAME/KEY:
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FEATURE:
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CITY: New
STATE: Ne
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Score 242.8; DB 18; Length 2084; Pred. No. 1.1e-51;

97.5%;

Query Match Best Local Similarity

Sequence 3, Application US/09327563B GENERAL INFORMATION:

RESULT 10 US-09-327-563B-3

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           Sequence 13, Application US/09545586
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Busgard-Frantzen Henrik
APPLICANT: Busgard-Frantzen Henrik
APPLICANT: Outtrup, Helle
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Hoeck, Lisbeth Hedegaard
TILLE REFERENCE: 5276.400-US
CURRENT FALING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
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ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/648,826
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09648826
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd Frantzen, Henrik
TITLE OF INVENTION: -Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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TYPE: DNA
; ORGANISM: B. amyloliquefaciens
US-09-545-586-13
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Best Local 3
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                                                     1 GCCCCGCACATACGAAAAGACTGGCTGAAAACATTGAGCCTTTGATGACTGATTTGG 60
   Gaps
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Pred. No. 1.1e-51;
0; Mismatches 2; Indels 0;
 2; Indels
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Sequence 31, Application US/09441313A
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Kjaerulff, Soren
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Andersen, Carsten
TITLE OF INVENTION: Alpha-amylase variants
FILE REFERENCE: 5709.200-US
CURRENT APPLICATION UNMBER: US/09/441,313A
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 31
LENGTH: 2084
 0; Mismatches
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Best Local Similarity 99.2
Matches 244; Conservative
Matches 244; Conservative
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OTHER INFORMATION: CDS
US-09-441-313A-31
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APPLICANT: Bisgard Frantsen, Henrik APPLICANT: Borchert, Torben Vedel TITLE OF INVENTION: Alpha-Amylase Mutants; FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/09/648,826A
CURRENT FILING DATE: 2000-08-25
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 2084
TYPE: DNA
ORGANISM: B. amyloliquefaciens
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/327,563
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38 475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECAX: 212-867-0123
TELECAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEDUENCE CHARACTERISTICS:
LENGTH: 2084 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
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FEATURE:
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Matches 244; Conservative
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US-09-648-826-3
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